

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2004, 11:50:08 ; Search time 114.64 Seconds

(without alignments)
2416.469 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675

Sequence: 1 MFGGKNIIEGALNTTGDLA.....LVFSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_podent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4675	100.0	878	10 Q42710	Q42710 cucumis sat
2	4672	99.9	878	10 Q42704	Q42704 cucumis sat
3	3657.5	78.2	877	10 Q42705	Q42705 cucumis sat
4	3038	65.0	873	10 Q93Y18	Q93Y18 corylus ave
5	2992.5	64.0	857	10 Q41238	Q41238 solanum tub
6	2862	63.8	860	10 Q43190	Q43190 solanum tub
7	2959	63.3	864	10 Q49150	Q49150 solanum tub
8	2948.5	63.1	862	10 Q43191	Q43191 solanum tub
9	2946	63.0	862	10 Q9FT17	Q9FT17 lycopersico
10	2942.5	62.9	862	10 Q9LEA9	Q9LEA9 prunus dulc
11	2941	62.9	861	10 Q24379	Q24379 solanum tub
12	2939	62.9	861	10 Q22508	Q22508 solanum tub
13	2936	62.8	861	10 Q3SC16	Q3SC16 solanum tub
14	2931.5	62.7	862	10 Q8W4X6	Q8W4X6 prunus dulc
15	2925	62.6	861	10 Q22507	Q22507 solanum tub
16	2917	62.4	861	10 Q43189	Q43189 solanum tub

ALIGNMENTS

RESULT 1

ID	Q42710	PRELIMINARY;	PRT;	878 AA.
AC	Q42710;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Lipoxigenase (EC 1.13.11.12).			
OS	Cucumis sativus (Cucumber).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid I; Cucurbitales; Cucurbitaceae; Cucumis.			
OX	NCBI_TaxID=3659;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cotyledon;			
RX	MEDLINE=97054584; PubMed=898881;			
RA	Hoehne M., Nellen A., Schwennesen A., Kindl H.;			
RT	"Lipid body lipoxigenase characterized by protein fragmentation, cDNA			
RT	sequence and by its very early expression during germination of			
RT	cucumber seeds.";			
RL	Eur. J. Biochem. 241:6-11(1996).			
DR	EMBL; X92890; CAA63483.1; -			
DR	P1R; S74207; S74207.			
DR	HSSP; P08170; 2SBL.			
DR	GO; GO:0005506; F:iron ion binding; IEA.			
DR	GO; GO:0016165; F:lipoxigenase activity; IEA.			
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR	GO; GO:0006118; P:electron transport; IEA.			
DR	InterPro; IPR000907; Lipoxigenase.			
DR	InterPro; IPR01024; Lipoxigenase_LH2.			
DR	Pfam; PF00305; lipoxigenase; 1.			
DR	Pfam; PF01477; PLAT; 1.			
DR	PRINTS; PR00087; LIPOXYGENASE.			
DR	SMART; SM00308; LH2; 1.			
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.			
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.			
DR	PROSITE; PS50095; PLAT; 1.			

17	2916	62.4	844	10 Q9SAP1	Q9SAP1 solanum tub
18	2911	62.3	862	10 Q43800	Q43800 nicotiana t
19	2895.5	61.9	865	10 Q93W22	Q93W22 gossypium h
20	2876.5	61.5	884	10 Q7X9G5	Q7X9G5 fragaria an
21	2876	61.5	857	10 Q8GV02	Q8GV02 brassica na
22	2813.5	60.2	859	10 Q42873	Q42873 lycopersico
23	2762	59.1	881	10 Q9M463	Q9M463 cucumis sat
24	2705	57.9	876	10 Q41430	Q41430 solanum tub
25	2692.5	57.6	866	10 Q39870	Q39870 glycine max
26	2677.5	57.3	854	10 Q9FNX7	Q9FNX7 arabidopsis
27	2677.5	57.3	858	10 Q9ZU05	Q9ZU05 persea aner
28	2663	57.0	865	10 Q24320	Q24320 phaseolus v
29	2653.5	56.8	882	10 Q9LUW0	Q9LUW0 arabidopsis
30	2649	56.7	859	10 Q43440	Q43440 glycine max
31	2640.5	56.5	858	10 Q04919	Q04919 vicia faba
32	2634.5	56.4	856	10 Q42780	Q42780 glycine max
33	2632.5	56.3	868	10 Q24470	Q24470 pisum sativ
34	2577	55.1	853	10 Q43446	Q43446 glycine max
35	2571	55.0	839	10 Q43438	Q43438 glycine max
36	2567	54.9	866	10 Q24295	Q24295 pisum sativ
37	2552.5	54.6	856	10 Q9M684	Q9M684 phaseolus v
38	2538.5	54.3	877	10 Q8S6D6	Q8S6D6 cryza sativ
39	2536.5	54.3	874	10 Q9FQF9	Q9FQF9 phaseolus v
40	2531	54.1	863	10 Q8S6B8	Q8S6B8 oryza sativ
41	2529	54.1	865	10 Q9FEQ3	Q9FEQ3 pisum sativ
42	2525.5	54.0	864	10 Q8W0V2	Q8W0V2 zea mays (m
43	2522.5	54.0	864	10 Q9AXG8	Q9AXG8 zea mays (m
44	2518.5	53.9	697	10 Q24377	Q24377 solanum tub
45	2507	53.6	870	10 Q7Y1F4	Q7Y1F4 oryza sativ

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KW Oxidoreductase.
SQ SEQUENCE 878 AA; 99768 MW; A92660AFA4D1ED3BE CRC64;

Query Match 100.0%; Score 4675; DB 10; Length 878;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIPLPAGESVFOINF 60
DB 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIPLPAGESVFOINF 60

QY 61 SNLLDNFTLLGGVSVFOLISATHTSNDSRGKNGKAYLERWLSIPLPAGESVFOINF 120
DB 61 SNLLDNFTLLGGVSVFOLISATHTSNDSRGKNGKAYLERWLSIPLPAGESVFOINF 120

QY 121 QWENFGFGPAFFIKNGHTSEFFLKSLTLDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180
DB 121 QWENFGFGPAFFIKNGHTSEFFLKSLTLDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180

QY 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKWDRIYDVYNDIADPDVGDHRPILG 240
DB 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKWDRIYDVYNDIADPDVGDHRPILG 240

QY 241 GTTEYPYPRRGRTGPRSRRDHNYESRLSPIMSLDIYVPKDNFGLKMSDFLGYYTKAL 300
DB 241 GTTEYPYPRRGRTGPRSRRDHNYESRLSPIMSLDIYVPKDNFGLKMSDFLGYYTKAL 300

QY 301 SISIKPGLQSIQFDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTLEDTPPLFKALVRNDG 360
DB 301 SISIKPGLQSIQFDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTLEDTPPLFKALVRNDG 360

QY 361 EKFLKFTPEVVYKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
DB 361 EKFLKFTPEVVYKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420

QY 421 TITEHIIKHGDLGLTVDSAMQNRLYIVDFHDLMPYLTRNATSTKYATRTLLLLKDD 480
DB 421 TITEHIIKHGDLGLTVDSAMQNRLYIVDFHDLMPYLTRNATSTKYATRTLLLLKDD 480

QY 481 GTLKPLVIELALPHFQDGLGAIKSLYPPAENGQKSIWLAKAYVTVDVGVHQLISHW 540
DB 481 GTLKPLVIELALPHFQDGLGAIKSLYPPAENGQKSIWLAKAYVTVDVGVHQLISHW 540

QY 541 LATHAVLEPFIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIBTHYPS 600
DB 541 LATHAVLEPFIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIBTHYPS 600

QY 601 KYSBELSILYKDWTFPQDALPNNLMKGLAVEDSSAPHGLRLILINDYPAVDGLDIWSA 660
DB 601 KYSBELSILYKDWTFPQDALPNNLMKGLAVEDSSAPHGLRLILINDYPAVDGLDIWSA 660

QY 661 IKTWVDYCCLYKDDNVAQNDVDFELQSWNBLREKGHADKKHEPWPMPQMTLSLIESCT 720
DB 661 IKTWVDYCCLYKDDNVAQNDVDFELQSWNBLREKGHADKKHEPWPMPQMTLSLIESCT 720

QY 721 TIITWASALHAANFQVPGYGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAFRLTICS 780
DB 721 TIITWASALHAANFQVPGYGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAFRLTICS 780

QY 781 ELQALVSIISIIELSKHASDVYILQORASIDWTSKDIALEAFKGNLFVEVNRIMERN 840
DB 781 ELQALVSIISIIELSKHASDVYILQORASIDWTSKDIALEAFKGNLFVEVNRIMERN 840

QY 841 KEVNLKNSGPNLPYTLVLPSSNEGLTGRGIPNSISI 878
DB 841 KEVNLKNSGPNLPYTLVLPSSNEGLTGRGIPNSISI 878

RESULT 2
Q42704
ID Q42704 PRELIMINARY; PRT; 878 AA.
AC Q42704;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LN Lipoxxygenase 1 (EC 1.13.11.12).
GN LOX1.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_taxid=3659;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Suvo; TISSUE=Germinating cotyledons;
RC MEDLINE=96061722; PubMed=7480330;
RA Matsui K., Tsuru B., Kajiwara T., Hase T.;
RT "Nucleotide sequence of a cucumber cotyledon lipoxxygenase cDNA
(GenBank U25058) (PGR95-044).";
RL Plant Physiol. 109:337-337(1995).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=Suvo; TISSUE=Germinating cotyledons;
RC Matsui K., Tsuru B., Kajiwara T., Hase T.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U25058; AAC61785.1; -.
DR HSSP; P08170; 2SBL.
DR GO; GO:0005506; F:Iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxxygenase_LH2.
DR InterPro; IPR001024; Lipoxxygenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00881; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR Oxidoreductase.
KW SEQUENCE 878 AA; 99784 MW; F219407ED7C269B8 CRC64;

Query Match 99.9%; Score 4672; DB 10; Length 878;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 877; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIPLPAGESVFOINF 60
DB 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIPLPAGESVFOINF 60

QY 61 SNLLDNFTLLGGVSVFOLISATHTSNDSRGKNGKAYLERWLSIPLPAGESVFOINF 120
DB 61 SNLLDNFTLLGGVSVFOLISATHTSNDSRGKNGKAYLERWLSIPLPAGESVFOINF 120

QY 121 QWENFGFGPAFFIKNGHTSEFFLKSLTLDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180
DB 121 QWENFGFGPAFFIKNGHTSEFFLKSLTLDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180

QY 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKWDRIYDVYNDIADPDVGDHRPILG 240
DB 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKWDRIYDVYNDIADPDVGDHRPILG 240

QY 241 GTTEYPYPRRGRTGPRSRRDHNYESRLSPIMSLDIYVPKDNFGLKMSDFLGYYTKAL 300
DB 241 GTTEYPYPRRGRTGPRSRRDHNYESRLSPIMSLDIYVPKDNFGLKMSDFLGYYTKAL 300

QY 301 SISIKPGLQSIQFDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTLEDTPPLFKALVRNDG 360
DB 301 SISIKPGLQSIQFDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTLEDTPPLFKALVRNDG 360

QY 361 EKFLKFTPEVVYKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
DB 361 EKFLKFTPEVVYKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
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QY 421 TITTEHIKHGLDGLTVDEAMKQNLXYVDFHDMPLVTRMNTSTTKYATRTLLLLKOD 480
DB 421 TITTEHIKHGLDGLTVDEAMKQNLXYVDFHDMPLVTRMNTSTTKYATRTLLLLKOD 480
QY 481 GTLAPLVIELALPHPOGDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGHOLISHW 540
DB 481 GTLAPLVIELALPHPOGDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGHOLISHW 540
QY 541 LHTHAVLEPFVIAHTRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHYS 600
DB 541 LHTHAVLEPFVIAHTRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHYS 600
QY 601 KYSNELSILYKDMTFDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVGLDLSWA 660
DB 601 KYSNELSILYKDMTFDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVGLDLSWA 660
QY 661 IKTWVQDYCYLYKDDNAVQNDFELQSWNELREKGHADKHEPWPVKMTLSSELIESCT 720
DB 661 IKTWVQDYCYLYKDDNAVQNDFELQSWNELREKGHADKHEPWPVKMTLSSELIESCT 720
QY 721 TIIMIASALHAAVNFQGYPIGGYILNRPPTTSRRMPVSGTAEBYKELESNEPEKAFRTICS 780
DB 721 TIIMIASALHAAVNFQGYPIGGYILNRPPTTSRRMPVSGTAEBYKELESNEPEKAFRTICS 780
QY 781 ELQALVSIIEILSKHASDEVILQORASIDWTSDKIALFAFEKFGKNLFEVENRIMERN 840
DB 781 ELQALVSIIEILSKHASDEVILQORASIDWTSDKIALFAFEKFGKNLFEVENRIMERN 840
QY 841 KEVNLKNSRGPVNLPLYLLPSSNEGLTGRGIPNSISI 878
DB 841 KEVNLKNSRGPVNLPLYLLPSSNEGLTGRGIPNSISI 878

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RESULT 3

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Q42705 PRELIMINARY; PRT; 877 AA.
ID Q42705
AC Q42705;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Suvo; TISSUE=Root;
RA Matsui K., Nishiooka M., Kajiura T., Hase T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U36339; AAA79186.1; -
DR PIR; T10085; T10085.
DR HSSP; P09186; 1LNH.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0001615; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR Oxidoreductase.
KW SEQUENCE
SQ 877 AA; 99393 MW; 35173589719FA33F CRC64;

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Query Match

Best Local Similarity

78.2%; Score 3657.5; DB 10; Length 877;

76.2%; Pred. No. 6.7e-265;

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Matches 671; Conservative 105; Mismatches 99; Indels 5; Gaps 4;
QY 1 MFGIGKNIIEGALNTTDLAGSVINAGNILDVRSSLGNGKIKGVILMRSNVLDFTFFH 60
DB 1 MFSIGKNIIEGALNTTDLAGSVINAGNIDQISNGGKIKGVILMRSNVMDFTFFH 60
QY 61 SNLONFTELLGGGVFSOLISATHISN-DSRGKVGKAYLERWLTISIPPLFAGESVPQIN 119
DB 61 SLLDNFTELLGGGVFSOLISATHISN-DSRGKVGKAYLERWLTISIPPLFAGESVPQIN 120
QY 120 FOWDENFGPGGAFFIKNGHTSEFFLKSLTLDVPGYGRVHFDCNSWVPSGYKKDRIF 179
DB 121 FWESEFGPGGAFFIKNGHTSEFFLKSLTLDVPGYGRVHFDCNSWVPSGYKKDRIF 180
QY 180 ANHYVLPSTPNPLKYREBELWNLURGDGTGERKWDRIYDYVDVNDIADPDVGHRPIL 239
DB 181 ANNYTLPSTPNPLKYREBELWNLURGDGTGERKWDRIYDYVDVNDIADPDVGHRPIL 238
QY 240 GGTVEYPRRGRTGRPRSRDRHYESRLSPIMSJDYVPKDNFEGHLMKMSDFLYTLKA 299
DB 239 GG-SQFPYPRRGRTGRPREWKSNSYERLPPVSGLNIVPRDENFGHLKLSDFLGFAKS 297
QY 300 LSISIKPGLQSIQDVTNPFNEFNCFEVDNLFERGFPIPFNAFKLTLEDTPPLFKALVRND 359
DB 298 LVATVQPALVNIIVDTFGFDFKQDVHNLVEGGLVPLDVFENLTQDTPPMFQELLRTD 357
QY 360 G-EKELKFTPEWVKDNKIGNSTDEEFAREMLAGNPILLIRLEAFPTSKLDPMYGNQ 418
DB 358 NDORFLKFPPOVNVKEDKPAWQTDDEFAREMLAGNPILLIRLEAFPTSKLDPMYGNQ 417
QY 419 NSTITEEHIKHGLDGLTVDEAMKQNLXYVDFHDMPLVTRMNTSTTKYATRTLLLLK 478
DB 418 HSKITEEDIKSGLEGLTVAEALNQRLXYLDHHDALMPYLRKINSTKTATRTLLLLK 477
QY 479 DDGTLKPLVIELALPHPOGDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGHOLIS 538
DB 478 NDGTLKPLVIELALPHPOGDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGHOLIS 537
QY 539 HMLTHAVLEPFVIAHTRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHY 598
DB 538 HMLTHAVLEPFVIAHTRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHY 597
QY 599 PKYSNWEJSSILYKDMTFDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVGLDLSW 658
DB 598 QSKYAMELSSYTYKEWNFTQALPVDLTKRGVAVEDPSPNGVKLLIEDYPFAVGLDLSW 657
QY 659 SALKTWQDYCYLYKDDNAVQNDFELQSWNELREKGHADKHEPWPVKMTLSSELIES 718
DB 658 STIKTWNTNYCSLYKDDSAIQNDVELQSWKEVREKGVKDKNETWPKQNFELVET 717
QY 719 CTIIWIASALHAAVNFQGYPIGGYILNRPPTTSRRMPVSGTAEBYKELESNEPEKAFRTI 778
DB 718 CTIIWIASALHAAVNFQGYPIGGYILNRPPTTSRRMPVSGTAEBYKELESNEPEKAFRTI 777
QY 779 CSELQALVSIIEILSKHASDEVILQORASIDWTSDKIALFAFEKFGKNLFEVENRIME 838
DB 778 NSMLQTLGVSLIIEILSKHASDEVILQORASIDWTSDKIALFAFEKFGKNLFEVENRIME 837
QY 839 RNKEVNLKNSRGPVNLPLYLLPSSNEGLTGRGIPNSISI 878
DB 838 RNKVDNLKNSRGPVNLPLYLLPSSNEGLTGRGIPNSISI 877

```

RESULT 4

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Q93YI8 PRELIMINARY; PRT; 873 AA.
ID Q93YI8
AC Q93YI8;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Corylus avellana (European hazel).

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Db 127 DVPHGKVFHVCNSWVYPSFRYKSDRIFFANQPYLPSETPELLAKYRENELLTLRGDGTG 186
Qy 211 ERKEDWRYDYVDYNDIADPDVGH--RPILGGTTEYPPRGSTGRPRSRDNYESRL 268
Db 187 KREAWDRYDYVDYNDLNGDQGEONVTTTGGGADYPPRRGTGPPPTKTDPKSESRI 246
Qy 269 SPIMSLDYVPKDNFGLKMSDFLGYTLKALSISIKPGLQSIKIDVTPNFDNFKEVDNL 328
Db 247 PLILSLDYVPRDERFGLKMSDFLTVALKSIQVFIPLPELHALFDGTPNEFDSFEDVLR 306
Qy 329 FERGPPIFN-AFKTLTIEDTPPLFKALVRNDGEKFLKFPPEVVKNKICGWSDEEFAR 387
Db 307 YEGGKTLFGGELFKALTAAPLEMMKELLRTDGEILRFPPLVVKDSKTAWRTDEEFAR 366
Qy 388 EMLAGNELLIRLEAFPPSTKLPNVYGNQNSITTEHIEKHGDLGLTVDEAMKONRLYI 447
Db 367 EMLAGVNPILIRLCEPPPKSLDPEAYGNQNSITTAHIEDKLDGLTVDEAMNNKLF 426
Qy 448 VDFHDLMPYITRNATSTKYATRTLLLLKDDGTLPVLTELALPHQDGLGALSILY 507
Db 427 LNHHDLVILYLRINTTTKYASRTLLFLQDNGSLKPLATELSLPHDPDGDQFGVISKY 486
Qy 508 FPAENGVOKSIWOLAKAVYVNDVGYHQLISHWLTHAVLEPPFVIATHRQLSVLHPHKL 567
Db 487 TPSQGVSESSIWOLAKAVAVNDVSGVHQLISHWLTHAVLEPPFVIATHRQLSVLHPHKL 546
Qy 568 LVPHYKDTMFINASARQVLINANGLIETHYPYSKYSMELSSILYKDWTFPDQALPNNLMK 627
Db 547 LYPHFRDTMFINAMARQILINAGVLESTVFPKSFAMEMSAVYKDWTFPDQALPADLVK 606
Qy 628 RGLAVEDSSAPHLRLINDYPPAVDGLDITMSAKTIVVODYCCLYKDDNAVQNDPELOS 687
Db 607 RGVAVEUSSPHGVRLIEDIPIYAVDGLIEMSAIKSWVTDYCSFYSGDSEIILKDELQA 666
Qy 688 WNNELREKGHADKHEPMPKQVOTLSBELIBSCITIIWIASALHAANVFGOPYGGYILNR 747
Db 667 WKELREVGHGDKKNPPWPEWETPQELIDSCITIIWIASALHAANVFGOPYGAYILPNR 726
Qy 748 PTTSRFRPEVGTAEYKELESNPKAFILRTICSELOALVSIISIIILSKHASDEVYLGQR 807
Db 727 PTVSRFRPEPGTPEYELKKNPKAFILRTITAOLOTLLGVSLTEILSRHTDEIYLGQR 786
Qy 808 ASIDWTSKIALAEAFKGNLFVENRIMERNKEVNLKNSGPNVLPYLLVPSSNEGL 867
Db 787 ESPWTKDKEPLAADFEGKLLDIEKQILQIRNGDNILTRSGVGNAPYLLPFTSBGGL 846
Qy 868 TGRGIPNSISI 878
Db 847 TKGIPNSVSI 857

RESULT 6

Q43190 ID Q43190 PRELIMINARY; PRT; 860 AA.
AC DT 01-NOV-1996 (TrEMBLrel. 01, Created)
CC K010165; Filipoxygenase activity; IEA.
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN POLX-2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_taxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ev. Superior;
RA K010165; Filipoxygenase activity; IEA.
RT "Potato Lipoxigenase Genes Expressed During the Early Stages of
RT Tubarization (Accession Nos. U60200 and U60201) (PGR96-065).";
RL Plant Physiol. 112:446-446(1996).
DR EMBL; U60201; AB67860.1; --

DR HSSP; P08170; 2SBL.
DR GO; GO:0005506; Piron ion binding; IEA.
DR GO; GO:0016165; Filipoxygenase activity; IEA.
DR GO; GO:0016491; Fioxidoreductase activity; IEA.
DR GO; GO:0006118; Pielection transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 860 AA; 96969 MW; 11FD0D769921053E CRC64;

Query Match 63.8%; Score 2982; DB 10; Length 860;
Best Local Similarity 63.8%; Pred. No. 2.7e-214;
Matches 553; Conservative 125; Mismatches 175; Indels 14; Gaps 5;

Qy 17 GDLAGSVINAGNILDVSSLOGNKKIKGVILMRNVLDFTFHSNLLDNFTTELGGVYS 76
Db 3 GOIVGGLI--GGH-----HDSKKVKTVMKKNALDFTDLAGSLDKLKEALGQKVS 53
Qy 77 FQLISATHT--SNDGRGKVGKAYLERWLTISIPPLFAGESVFOINQWDENFGFPFAPFI 134
Db 54 FQLISSVQSDPANGQKHSNAYLENFLFITPLAAGETAAGVTDFWNEEGVFGARTII 113
Qy 135 KNGHTSEFPKLTLDDVPGYGRVHFDNCNSWYPSGRYKXDRIFFANHYVLPSTPNPLR 194
Db 114 KNTHINEFFKLTLTEDVPHGKHFVNCNSWYPSFRYKSDRIFFANQPYLPSETPELLR 173
Qy 195 KYREELNLRGDGGERKEWDRIYDYVNDIADPDVGH--RPILGGTTEYPPRGQR 252
Db 174 KYREELLTLRGDGTGKEAWDRIYDYVNDLGNPDQKENVRTLGGSDADYPPRGQR 233
Qy 253 TGRPSRRDHYESRLSPIMSLDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLQSI 312
Db 234 TGRPPTRTDPKSESRIPLTSLDIYVPRDERFGLKMSDFLTVALKSIQVFIPLPELHALF 293
Qy 313 DVTNREFDNFKVDNLFERGPPIPN-AFKTLTIEDTPPLFKALVRNDGEKFLKFPTEV 371
Db 294 DGTNREFDSFEDVLRLEGGRILPQGLFKALTDAIPELMIRELRLTDEGILREPTPLV 353
Qy 372 VKDNKIGSTDEEFAREMLAGNPLILIRLEAFPPSTKLPNVYGNQNSITTEHIEKHGL 431
Db 354 IKDSKTAWRTDEEFAREMLAGVNPILIRLEAFPPSTKLPNVYGNQNSITTEHIEKHGL 413
Qy 432 DGLTVDEAMKQNLIVDFHDLMPYITRNATSTKYATRTLLLLKDDGTLPVLTELALH 491
Db 414 DGLTVDEAMNNKLPILNHHDLVILYLRINTTTKYASRTLLFLQDNGSLKPLATELS 473
Qy 492 LPHPOGDOLGALSILYKLVPAENGVOKSIWOLAKAVYVNDVGYHQLISHWLTHAVLEP 551
Db 474 LPHPOGDQFGVTSKYVTSQGVSESSIWOLAKAVAVNDVSGVHQLISHWLTHAVIEP 533
Qy 552 IATHRQLSVLHPHKLPHVYKDTMFINASARQVLINANGLIETHYPYSKYSMELSSILY 611
Db 534 IATHRQLSVLHPHKLPHVYKDTMFINASARQVLINANGLIETHYPYSKYSMELSSILY 593
Qy 612 KDWTFPDQALPNNLMKRGVAVEDSSAPHLRLINDYPPAVDGLDITMSAKTIVVODYCC 671
Db 594 KDWTFPDQALPADLVKRGVAVEDSSPHGVRLIEDIPIYAVDGLIEMSAIKSWVTDYCS 653
Qy 672 YYKDDNAVQNDPELOSWMNELREKGHADKHEPMPKQVOTLSBELIBSCITIIWIASALHA 731
Db 654 YXGDEEILKDELQAWKELREVGHGDKKNPPWPEWETPQELIDSCITIIWIASALHA 713
Qy 732 AVNFGOPYGGYILNRPPTSRFRPEVGTAEYKELESNPKAFILRTICSELOALVSIISII 791
Db 714 AVNFGOPYGAYILNRPPTSRFRPEVGTAEYKELESNPKAFILRTICSELOALVSIISII 773


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DR Pfam: PF01477; PLAT; 1.
DR PRINTS: PR00087; LIPOXYGENASE.
DR SMART: SM00308; LH2; 1.
DR PROSITE: PS00711; LIPOXYGENASE_1; 1.
DR PROSITE: PS00081; LIPOXYGENASE_2; 1.
DR PROSITE: PS50095; PLAT; 1.
DR OXidoreductase.
SQ SEQUENCE 862 AA; 97778 MW; 946679AF56041E89 CRC64;

Query Match
Best Local Similarity 63.1%; Score 2948.5; DB 10; Length 862;
Matches 534; Conservative 138; Mismatches 168; Indels 5; Gaps 3;

QY 39 GNKIKGVILMSNVLDPFEHNSLNDFTFELGGVSPQLISATH--SNDSRGKGVNK 96
DB 18 GKVGKTVILMKKVLDFNDVNASLLDGLVFLGKRVSLQLISVHADPGNSLQKSNP 77
QY 97 AYLERLWLTSPPLPAGESVQINFQWENFPGGPAFFIKNGHTSEFFLKSLTLDVPGY 156
DB 78 AYLERLWLTGTSVAGESAFDFTDDEIDIGVGAFIINNFHNEFYLSLTLEDVPHG 137
QY 157 RVHFDGNSWVPSGRYKDRIFFANHVLPSTQNPLEKRYEELWNLRGDGTGERKWD 216
DB 138 NVHFCVNSWVPKAKYKRIFFANQVLPGETPEPLRYREKELNLRGNKGLBEWD 197
QY 217 RIYDVVNDIADPDVGDH--RPILGGTTEYPYPRRGTRPRRRDHNYSRLSPIMSL 274
DB 198 RYDYVALYNDLGDPEKQYARTILGSAEYYPARGRTGRKPKADPKSESRIPLMSL 257
QY 275 DIYVKDENFGLKMSDFLYTLKALSISIKPGLQSIQDVTNPFEDNFKVDNLFERGF 334
DB 256 DIYVPRDRFGRHKLSDFTLVALSIVQFLPEFOALFDSFTDFDSEFVLYKLYEGGI 317
QY 335 IPFNAP-KTLTDELTTPPLFKALVRNDGKFLKFTPEVVKDKNGKWSDEEFAREMLAG 393
DB 318 LPQGFPLKALTDSPLEILKEIRTDGSGKFKFTPTQVIQEDKSWRTDEEFAREMLAG 377
QY 394 NPLIRLEAPPPSKLPDNYGNQNSTITBEHKLHGLDGLTVDKAMQNLYIVDFHDA 453
DB 378 NPVILSRLOEPFPKSQLDSSEYVGNQNSTITKEHIENTLDGLTIDDAIKNRLYILNHI 437
QY 454 LMPYLTRNATSTKYATRTLLKDDGTLKPLVIELALPHQDGLGALSKLYFPAENG 513
DB 438 LMPYVRINTNKLKASRTLLFLQDDGTMPVAIELSLPHDPDGLQAVSKVTPADQG 497
QY 514 VOKSIWQLAKAVTVNDVGVHQLISHWLHHTHAVLEPPVIAHRLQSLVLPHTKLLVPHY 573
DB 498 VEGSIWQLAKAVVANDSGVHQLISHWLNTHAATEPFVIATNRQLSVLPHTHKLHPFR 557
QY 574 DTMFINASAROVLINANGLIETHYPSKYSNELSILYKDWTFPDQALPNNLMKRGAVE 633
DB 558 DTMNINARQLLINAGVLEMTVFPKAYAMSAVYKSVVFPQALPADLIRGVAVE 617
QY 634 DSSAPHGLRLILNDYFPAVDGLDLSAIKTWVQDYCYLLYKDDNAVONDFELQSWNELR 693
DB 618 DSSPHGVLLIQDYPAVADGLIWSAISKSVTEYCNFYKSDLVKDNELQAWKELR 677
QY 694 EKHADKKEHPKMQTLSELISCTIIIIWASALHAANVFGYPGGYILNRPPTSR 753
DB 678 BEGHDKKDEPWPQKQTRQLKDSCTIIIIWASALHAANVFGYPYAGYLPNRPPTSR 737
QY 754 FMPVEGTAEYKELESNPKAFRLTICSELQALVSIISIELSKHASDEVYLGQRASDWT 813
DB 738 FMPPEGTPEYELKTNPKAYLKITPQLQTLIGLSIELSRHASDEIVLQORDSEWT 797
QY 814 SDKIALEAFKGNLFFVENRIMERNKENVLNKRSFVNLPYTLVPSNEGTLGRGIP 873
DB 798 KDQEFIAAFERFKKLSIEDQIIQMNGDKKWKNSRGPVNVPTLLPPTSEQGLTKGIP 857
QY 874 NSISI 878
DB 858 NSVSI 862
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Db 426 RLFLINHHDIIMPVYRRINTTNTKMATRLLFLQDDGTLKPLAIELSLPHDPDQFGA 485
Qy 503 ISKLYFPAENGQKSIWOLAKAYTVNDVGVHQLISHWLTHAVLEPFIATHRQLSVLH 562
Db 486 VSEVFTSDQGVESIWOLAKAYAAVNDVGVHQLVSHWLNTHVIEPFIATNRQLSVLH 545
Qy 563 PIHKLIVPHYKDTWPFINASQVILINANGLIETHTHYSKYSMELSSILYKDWTFPDQALP 622
Db 546 PIHKLILPHFRDTWMINALAQILINGGLLELTVFPKYSMELSSVYIKDWTFPEQALP 605
Qy 623 NNLKMRGLAVDSAPHGRLRLINDYPPAVDGLDIWSAIIKTWQDYCCLYYKODNAVQND 682
Db 606 ADLIRGVAVDSNSPHGRVLLIQDYPAVDGLSIWSAIIKSWTEYCNYYKSDDAVQKD 665
Qy 683 FELQSWNELREKGHADKHPWPMPKMTLSIELSCTTIWIASALHAAVNFGQYPIYG 742
Db 666 AELQAWKELREEGHDKKBPWPMPQMSVQELIDSCTTIWIASALHAAVNFGQYPIYG 725
Qy 743 YILARPPTSRPMPBPVGTAEYKELESNPEKAFLETICSELOALVSIISIHELKSHASDEV 802
Db 726 YLPNPTTSRPMPPBPVGTAEYKELESNPEKAFLETICSELOALVSIISIHELKSHASDEV 785
Qy 803 YILQASIDWTSKIALAFKFGKQNLPEVENRIMERKE-VNLKNSRGPVNLPTLLVP 861
Db 786 YLGQDSPEWTKQBPSPAFERFGKLGIEDRIIQMGNDNQKNSRGPVNLPTLLFP 845
Qy 862 SSNEGLTGRIPIINSISI 878
Db 846 TSEGLTGKIPNSVSI 862

RESULT 10
Q9LEA9 PRELIMINARY; PRT; 862 AA.
ID Q9LEA9
AC Q9LEA9
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OC NCBI_TaxID=3755;
RN [1]_TaxID=3755;
RP SEQUENCE FROM N.A.
RC STRAIN=Scv. Scorza verde;
RX MEDLINE=21153257; PubMed=11231304;
RA Mita G., Gallo A., Greco V., Zasiura C., Casey R., Zacheo G.,
RA Santino A.;
RT "Molecular cloning and biochemical characterization of a lipoxigenase
RT in almond (Prunus dulcis) seed.";
RL Eur. J. Biochem. 268:1500-1507(2001).
RR EMBL; AJ404331; CAB94852.1; -.
DR HSP; P08170; 2SBU.
DR GO; GO:0005506; P:iron ion binding; IEA.
DR GO; GO:0016165; P:lipoxigenase activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SEQUENCE 862 AA; 980:9 MW; EE078F795F435626 CRC64;
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Query Match 62.9%; Score 2942.5; DB 10; Length 862;
Best Local Similarity 62.2%; Pred. No. 2.5e-211;
Matches 534; Conservative 143; Mismatches 173; Indels 9; Gaps 3;

Qy 29 NTLDRVSSLGNN-----KIKGVILMRSNVLDFTEFHNLLDNFTLGGGVSPQLISAT 83
Db 4 NLFDKITGOEQNGKNSRKIKGVILMKXNVLDNFDFNASVLDVRVHLLGQGVSLQLISAD 63
Qy 84 H--TNSDRSGKVGKAYLERMLTSPPLPAGESVFPQNFQWDENFPGFCAFIKNGHTSE 141
Db 64 HGDSENGFKGLGEPAYLEDWITTTPLTIGDSAYKVTDFWEEIEIGVPGAILIKNHSE 123
Qy 142 FFLKSLTLDVDPVGRVHFDGNSWYPSGRYKDKRIFFANHVYLPSONPRLRYREBEL 201
Db 124 FFLKTTITLDEVPRGRVHFVCSWVYPAKTKRQVFFVNTFLPSETPFLPKRYREBEL 183
Qy 202 WNLRGDGTGERKEWDRIYDYVNDIADPDVGDH--RPILGTTTEYPYPRGRTGRPSR 259
Db 184 VHLRGDGKGLQWDRVYDAYVNDLGNPDKPKYARPTLGGSSBYYPYPRGRTGRPPTK 243
Qy 260 RHNYESRLSPIMSLDIYVPKDNFPHLKMDFGLYTLKALSISIKPGLSQIFDVTPNEF 319
Db 244 TDSNESRIPPLMSLNIYVPRDERFGLKLSDFLALAKSIVQFIRPELEALFKTPNEF 303
Qy 320 DNFKVDNLFERGFPIPFNAFKTLTDELTPPLFKALVENDGEKFLKFTPEVVKDNKIGW 379
Db 304 DSLEDVLKLYGGIPLPESGLLKIGDNIPAEMLKBEIPRTDGAQLRFPMPQVIEEDKSAW 363
Qy 380 STDEPFAREMLAGNPPLIRLEAPPTSKLDPNVYQNQSTITEEHKKGDLGLTVDEA 439
Db 364 RTDEPFAREMLAGVNPVNISLQEPFPASKLDPKVYGDTSRTIQDIGNKLDGLTVDEA 423
Qy 440 MKONRLYIVDFHDALMPYLTRMNATSTKYATRTLLLLKDDGDTLKLPLVIELALPHQDQ 499
Db 424 LKONKFLIHDHALMPYLRLINSTNKIYASRTVLFLKSDGTLKPLVIELSLPHPDGQ 483
Qy 500 LGAISKLYPFAENGQKSIWOLAKAYTVNDVGVHQLISHWLTHAVLEPFIATHRQLS 559
Db 484 FGRISKVYTPAEEGVESIWOLAKAYVAVNDVGVHQLISHWLNTHAVCEPVVIATNRQLS 543
Qy 620 ALPNMLKREGLAVEDSSAPHGRLRLINDYPPAVDGLDIWSAIIKTWQDYCCLYYKDDNAV 679
Db 604 ALPADLINRGVAVKQANSPHGLRLIIDDYPAVDGIEIWFATKWVEDYCSFYKTDII 663
Qy 680 QNDFELQSWNELREKGHADKHPWPMPKMTLSIELSCTTIWIASALHAAVNFGQVP 739
Db 664 QNDIELQSWNELVEEGHDKKBPWPMPQMSVQELIDSCTTIWIASALHAAVNFGQVP 723
Qy 740 YGYIINRPTTSRRRPMPEVGTAEYKELESNPEKAFLETICSELOALVSIISIHELKSHAS 799
Db 724 YAGYLPNRPPTISRKFMPEKGTPEYKELESNPEKAFLETICSELOALVSIISIHELKSHAS 783
Qy 800 DEVYLQASIDWTSKIALAFKFGKQNLPEVENRIMERKEVNLKNSRGPVNLPTLL 859
Db 784 DEVYLQORDTPPTWATDEPLKAFKFGKLAIEDRIITRMNDEKLKRVGVPKPYTLL 843
Qy 860 VPSNNEGLTGRIPIINSISI 878
Db 844 PFTSEGLTGRIPIINSVSI 862

RESULT 11
Q24379 PRELIMINARY; PRT; 861 AA.
ID Q24379
AC Q24379;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
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DE Lipoxigenase (EC 1.13.11.12).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tuber;
RX MEDLINE=96355454; PubMed=8702864;
RA Royle J.N., Vancannett G., Perez A.G., Sanz C., Stormann K., Rosahl S.,
SA Sanchez-Serrano J.J.;
RT "Characterization of three potato lipoxigenases with distinct
RT enzymatic activities and different organ-specific and wound-regulated
RT expression patterns.";
RL J. Biol. Chem. 271:21012-21019(1996).
DR EMBL; X95513; CAA64766.1; -;
DR HSSP; P08170; 28BL.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016185; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 861 AA; 97067 MW; 25783F32C69BFA26 CRC64;

Query Match 62.9%; Score 2941; DB 10; Length 861;
Best Local Similarity 64.6%; Pred. No. 3.2e-211;
Matches 545; Conservative 118; Mismatches 175; Indels 6; Gaps 4;

QY 41 KIKGKVLMSNVLDFTFHSNLDNFTTELLGGVSVFOLISATH--TSNDRGRKVGKAY 98
DB 18 KLGTVVMNMKNALDFTDLGSLTKAFELGQTVFSPQLISSVQGDPTNGLQGHNPAY 77
QY 99 LERWLTSPPLFAG-ESVFQNFOWDENFGPPGAFKNGHTSEFFLKSITLDDVPQYGR 157
DB 78 LENSFLITPLTASSETAFGTFPWNHEFGVGFALIKNTINEFFLKSITLDDVPNHGK 137
QY 158 VHFPCNSWVPSGRYKXDRIFFAHNVLPSTQPNPLRYEEELWNLRGDTGERKEWDR 217
DB 138 VHFVCSNVVPSRYKSDRIFPFVQNPYLPKSTPELLRKYRENEILLTRGGDTGKREAWDR 197
QY 218 IYDYDVNDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPRGRDHVSRSLSPMSLD 275
DB 198 IYDYDINDLNGDEGENVTKTGGSAEYPYPRGRGTGRPTKTDPKSESRIPLILSLD 257
QY 276 IYVPKDNFGLKYSDFLYTLKALISIKPGLQSFIDVTPNEFDNFKNFVDNLFERGFPI 335
DB 258 IYVPRDERFGLKWSDFLYTALKSIVQFILPELHALFDGTPNEFDSPEVDLRLVEGGIKL 317
QY 336 PFN-AFKTLTLEDLPPELKAIVRNDGKFLKPTTPEVVKNKIKGWSDEFEAREMLAGPN 394
DB 318 PGGELFKALTAAPLEMIRELRDGTGGILRFPPPLVKDKSTAWRTDEFEAREMLAGVN 377
QY 395 PLLIRRLAEAPPSTKLDPNVGNQNSITTEHIXKHGDLGTLTVDEAMQNQLYIVDFHDAL 454
DB 378 PVILSRLOEFPFKSLDPEAGNQNQNSITAEHIEDKLDGLTVDEAMNNKFLINHHIDL 437
QY 455 MPYTRMNTATKTYATRTLLLLKDDGTLKPLVIELALPHPGQQLGAISKLFPFAENG 514
DB 438 IPEYLRINNTTKTYASTLLFLQNGSLKPLATELSLPHPDGQFGVTSKVTTPSDQV 497
QY 515 QKSIWQLAKAYVYVNDVGYHQLISHWLHTHVALEPFIATHRQLSVLHPHKLAVPHYKD 574

DB 498 ESSIWQLAKAYVAVNDSGVHQLISHWLHTHVALEPFIATHRQLSVLHPHKLAVPHYKD 557
QY 575 TWFINASROVLINAGLIEHTHYPSKYSMELSSILYKDWTFPDQALPNMLKRGVAVED 634
DB 558 TWNIWAMARQILINAGVLESIVFQSKFAMENASVAVKDWTFPDQALPADLVKRGVAVED 617
QY 635 SSAPHGLRLINDYPAVDGLDWSAIKTWQDYCYCLYYKDDNAVQNDVFELOSWMNLE 694
DB 618 SSSPHGVRLIEDYPAVDGLDWSAISKWSVSDYCSFYVYGSDEELKQNELQAMWKELE 677
QY 695 KGHAKKKEPWPKNQTLSELIESCTTIWTSALHAHVNFEGYPGVYLLNRPVTSRRF 754
DB 678 VGHGDKKKEPWPKNQTLSELIESCTTIWTSALHAHVNFEGYPGVYLLNRPVTSRRF 737
QY 755 MPEVGTAEYKELESNPEKAFRTICSELQALVSIISILSKHSDVYLLQGRASIDWTS 814
DB 738 MPEPGTPEVEELKKNPKDRAFLTKITAIQTLGLVSLIEILSRHTTDEIVLQGRESPEWTK 797
QY 815 DKIALEAEKFKGNLFEVENRIMERKENVLNKRGSPVNLPTLLVSPNSGLTGRGIPN 874
DB 798 DKEPLAFAFDKFGKLTDEKQIQRNGNLTNRSGPVNAPVYLLFTPTSEGLTGKIPN 857
QY 875 SISI 878
DB 858 SVSI 861

RESULT 12
O22508 PRELIMINARY; PRT; 861 AA.
AC O22508;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Lipoxigenase.
GN PLOX2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lehmi Russet; TISSUE=Tuber;
RA Fidansef A.L., Bostock R.M.;
RT "Solanum tuberosum (Lehmi Russet) lipoxigenase (plox2) mRNA, complete
RT cds.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF019614; AAB81595.1; -;
DR HSSP; P09186; 1LNH.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016185; F:lipoxigenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
SQ SEQUENCE 861 AA; 97020 MW; 92C31F6EAF55PB58 CRC64;

Query Match 62.9%; Score 2939; DB 10; Length 861;
Best Local Similarity 63.9%; Pred. No. 4.5e-211;
Matches 544; Conservative 124; Mismatches 173; Indels 10; Gaps 5;

QY 38 GGN----KIKGKVLMSNVLDFTFHSNLDNFTTELLGGVSVFOLISATH--TSNDRGR 91
DB 11 GGHDSKVKYGVVVMKNVLDFTDLASSLTGKIFDLVGLQKVSFOLISSVQGDPTNGLQG 70

Qy	92	KVGNKAYLGRWITSIPPLFAG-ESVQINQFOWDENFPGPAFFIKNGHTSEFFPKLSITLD	150
Db	71	KHNPAYLNSLFTPLTAGSETAFGVTTFDWNBEFGVGAFIKNNWHITFEFFKLSITL	130
Qy	151	DVPGYGRVFDNCNWSVPSGRVKKDRIIPFANHVIYPSQTNPLRKYKEEELMNLRGDGTG	210
Db	131	DVPHGKGVFCNWSVYPSLNYKSDRIIPFANQVYLPSETPELLKRYRENEELLTLRGDGTG	190
Qy	211	ERKEWDRIYDYVDYNDIADPDVGDH--RPILGGTTEYPYPRRGRTGPRSRRDHNTYESRL	268
Db	191	KREAWDRIYDYINDLGNPDQCKENWRTTLGGSAAEYYPARGRTGPRPTKDPKVKSI	250
Qy	269	SPTKSIDIYVPKDNFPHLKMDSFLGYTLKALSISIKPGLOSFDVTPNPFDFNKEVDNL	328
Db	251	PLLSLDIYVPKDRFPHLKMDSFUYALKSIVGFIPELHALFDGTPNPFDFSFEDVLR	310
Qy	329	FERGFPIPN-AFKLTUTDLTPPLFKALVRNDGKFLKFTTPEVVKNDKNKGWSTDEBEAF	387
Db	311	YEGGILKPOGLPFLKATAAIPLEMIRELLRTDGGILLRFPTELVIKDSKTAWRTDEEAF	370
Qy	388	EMLAGNPILLIRLEAFPTSKLDPNVYGNQNSITTEHKKHGLDGLTVDKAMQNRLEYI	447
Db	371	EMLAGNPTIIISRLQFFPKSKLDEAYGNQNSTIAEHIEDKLDGLTVDKAMNNKLEFI	430
Qy	448	VDPHALMPLYLRMNATSKTYATRTLLLLKDDGTLKPLVTELALPHPOQDQLCAISKLY	507
Db	431	LNHHVDVIIPLYRINTTITKYASRTLLFQONGSLAPLALIELSLPHPDGDPGVTSKYV	490
Qy	508	FPAENGQKSIWOLAKAYVTVNDVGYHQLISHWLTHAVLEPPVIATHROLSLVHPHKL	567
Db	491	TPTDQGVESSIWOLAKAYVAVNDTGVHQLISHWLNTHAVIEFPVIATNRQLSVLHPHKL	550
Qy	568	LVPHYKDTWFINASARQVLINANGLIETHYPSKYSMELSSILYKDWTFPDQALPNNLAK	627
Db	551	LYPHFDTWNINASARQILVNAAGVLESTVQSFAMEMSAVTVKOWFFDQALPADLVK	610
Qy	628	RLGAVEDSSAPHGLRLINDYFPAYDGLDIWSAIKTWQDYCCLYKXKDNVAVNQDFELOS	687
Db	611	RGVAVEDSSPHGVRLITIEDYPAVDGLEIWSAIKSWTVDYCSFYGSDEILKDNELQA	670
Qy	688	WNNELREKHADKQHPWPKMOTSELIESCTTIIMTASALHAANVFGQYPVGGVILNR	747
Db	671	WKKLEVEVGHGDKQNEPWWPEMKTPEQLIDISCTTIIMTASALHAANVFGQYPVAGVLPNR	730
Qy	748	PTTSRRFMEPVGTABYKELESNPKAFRLTICSELQALVSGISIIELSKHASDEVYLGOR	807
Db	731	PTVSRREFPEPGTPEYELKRNPKAFKTTIAQLQTLGLVSLVEILSRHTTDEIYLGOR	790
Qy	808	ASIDWTSKIALAEAKKQGNLFEVENRIMPRNKEVNLKORSQPVNLPYTLVPSSNEGL	867
Db	791	ESPEWTKDEPLAADFQKGLTDIEKQIIORNGENTILNRSQGVNAPYTLFPPTSEGL	850
Qy	868	TGRGIPNSISI 878	
Db	851	TGKIPNSVSI 861	
RESULT 13			
Q9SC16			
ID	Q9SC16	PRELIMINARY; PRT; 861 AA.	
AC	Q9SC16;		
DT	01-MAY-2000 (T-EMBLrel. 13, Created)		
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Lipoxygenase (EC 1.13.11.12).		
GN	LOX1-ST-2.		
OS	Solanum tuberosum (Potato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	lamiales; Solanales; Solanaceae; Solanum.		
OX	NCBI_TaxID=4113;		
RP	[1]		
RP	SEQUENCE FROM N.A.		

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Db 611 RGVADESSPHGVRLIEDYPAVADGLEIWSAISKSWTDYCFYGSDEILKDELQA 670
Qy 688 WNNELREKGGHADKHEPWPQWOTLSLIESCTIIWIASALHAANFGOPYGGYILNR 747
Db 671 WVKELREVGCDKKNBFWPEMKTPQELIDSCITIIWIASALHAANFGOPYAGYILPN 730
Qy 748 PTTSSRRFPEVGTAEYKELESNPEKAFRTICSELQALVSISIEILSKHASDEVYLGOR 807
Db 731 PTVSSRRFPEVGTAEYKELESNPEKAFRTICSELQALVSISIEILSKHASDEVYLGOR 790
Qy 808 ASIDMTSDKALEAFKFEKGNLFEVENRIMERNEKVNLRSGPVNLPYTLIYVSSNEGL 867
Db 791 ESPWTOKDPLAADFRRGKXLDIEKQIIQRNGDNLITNRSFVNAPYTLIYVSSNEGL 850
Qy 868 TGRGIPNSISI 878
Db 851 TGKGIPIVSVSI 861

RESULT 14
Q8W4X6
ID Q8W4X6 PRELIMINARY; PRT; 862 AA.
AC Q8W4X6;
DT 01-MAR-2002 (TremBrel. 20, Created)
DT 01-MAR-2002 (TremBrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN Lox.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Scorza verde;
RA Mita G., Gallo A., Fasano P., Zasiura C., Casey R., Santino A.;
RT "Molecular cloning of an almond lipoxigenase gene expressed during the
early stages of seed development."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ418043; CAD10779.2; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR KX Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 862 AA; 97751 MW; 3FAC9D205DCBC131 CRC64;
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Query Match 62.7%; Score 2931.5; DB 10; Length 862;
Best Local Similarity 61.9%; Pred. No. 1.6e-210;
Matches 532; Conservative 144; Mismatches 174; Indels 9; Gaps 3;

Qy 29 NILDRV-----SSLGNNKKGKVIIMRSNVLDFTEPHSNLLDNFTLLGGVGFQILISAT 83
Db 4 NLFDKITQEQNGKNGRKIKGTIVLMKKNVLDNFDFNASVLDVRVHLLGGVSLQILISAD 63
Qy 84 H--TSNDSRGKGNKAYLERWLTSPPLFAGESVQINFDNDNFGPPGAFITNGHTSE 141
Db 64 HGDSENGFKGKGLGPAYLEDWITITLTVDGSAVNVTFDWEIEIGVPGAILKNNHSE 123
Qy 142 PFLKSLTLDVPGVGRVHFDGNSVWVPSGRYKDKRIFFANHVLPSTNPLPKYREEL 201
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Db 124 PFLKTVTLIEDVPREGRVHFVCNWSVYPAEKYTKORVFFVNKTFLPSETPLPLRKYREEL 183
Qy 202 WNLRGDGTGERKEWDRIYDYVDYNDIADPDYGDH--RPILGTTPEYPRGRGTRPSRSR 259
Db 184 VHLRGDGGKEQEWDRVYDAYYNDLGNPDKSGKYARPTLGGSSGYPTPPRGTRGPATK 243
Qy 260 RDHYESRLSPIMSDIYVPKDNFNGHLMKSDFLGYTLTKALSISIKPGLQSFIDVTPNEF 319
Db 244 TDPNSESRIPLTMSLVNVPRDERFHLKLSDFLAYALKSIVQFIRPELEALFDPKTFNEF 303
Qy 320 DNFKVDNLPFERGFIPFNAKTLTDLTPPLKALVENDGKELKPTPEVVDKNKIGW 379
Db 304 DSFEDVLKLYTGGIPLPEGLLKIDGNIPAEMLKEIFRTDGAQLLRFPPMPOVIEDKSAW 363
Qy 380 STDEEFAREMLAGNPLLRLEAPPPSTKLDPNVYGNQNSTITEEHKKGIDGTVDEA 439
Db 364 RTDEEFAREMLAGVNPVNISLLQEPFPASKLPKPYGQTSRITTEQDIGNKLDGLTVHEA 423
Qy 440 MKQNELIYVDFHDALMPYLTRMNATSTKYATRILLLLKDDGTLKPLVIELALPHPDQDQ 499
Db 424 LKQNKLFILDHHDALMPYLRRINSTSNKIYASRTVFLKSDGTLKPLVIELSLPHPDQDQ 483
Qy 500 LGAIKSLYFPAENGVOYKSIWOLAKAYVTVDVGVHQLISHWLHTHAVLEPFIATHROLS 559
Db 484 FGRISKVYTPAEVGEVGSIQWLAKAYVAVDSGVHQLISHWLHTHAVCEPVVIATNROLS 543
Qy 560 VLHPHKLILVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMELSSILYKOWTFPDQ 619
Db 544 VVHPYIKLLHPHFRDTMFINAFARQIVINAGGILETTVPFSRYAMELSSVYKOWVTFEQ 603
Qy 620 ALPNMLKRGGLAVEDSSAPHGLRLILINDYPPAVDGLDIWSAIKTWQDYCCLYYKDDNAV 679
Db 604 ALPDLILKRGVAVKANSFPHGLRLILIEDYPYAVDGLIWFALKIWKVEDYCFYKTDII 663
Qy 680 QNDFELQSWNELREKHADKHEFPWPQMTLSLIESCTIIWIASALHAANFGOPY 739
Db 664 QSDTELQSWKXELVEEGHKKDPEWPKMQTRDELVETCTIIWIASALHAANFGOPY 723
Qy 740 YGGYILNRPPTTSRRPEVGTAEYKELESNPEKAFRTICSELQALVSISIEILSKHAS 799
Db 724 YAGYILNRPPTTSRRPEVGTAEYKELESNPEKAFRTICSELQALVSISIEILSKHAS 783
Qy 800 DEVILGORASIDWTSKIALBAFAKFGKFNLFENRIMERNEKVNLRSGPVNLPYTLI 859
Db 784 DEVILGQRDTPWTADTEPLKAFKFGKLAIEDRTSMNDEKLNKRVGVKVPYTLI 843
Qy 860 VPSSNEGLTGRGIPNSISI 878
Db 844 FPTSGLTGRGIPNSVSI 862

RESULT 15
O22507
ID O22507 PRELIMINARY; PRT; 861 AA.
AC O22507;
DT 01-JAN-1998 (TremBrel. 05, Created)
DT 01-JAN-1998 (TremBrel. 05, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Lipoxigenase.
GN FLOXL.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lehmi Russet; TISSUE=Tuber;
RA Fidantseef A.L., Boscock R.M.;
RT "Solanum tuberosum (Lehmi Russet) lipoxigenase (plox1) mRNA, complete
cds."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF019613; AAB81594.1; -.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2004, 12:03:09 ; Search time 139.206 Seconds
(without alignments)
1971.379 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675

Sequence: 1 MFGIGKNIIEGALNTGDLA.....LVPSNGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1285345 seqs, 31250633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	3933	84.1	880 14	US-10-059-909-12
2	3011.5	64.4	859 10	US-09-978-522-3
3	2995.5	64.1	862 10	US-09-978-522-1
4	2929	62.7	887 12	US-10-425-114-54449
5	2795	59.8	857 12	US-10-424-599-215976
6	2795	59.8	860 12	US-10-425-114-45769
7	2795	59.8	863 12	US-10-425-114-54429
8	2795	59.8	863 12	US-10-425-114-55253
9	2791	59.7	857 10	US-09-751-687-17
10	2742.5	58.7	826 12	US-10-424-599-215973
11	2742.5	58.7	832 12	US-10-425-114-45631
12	2713.5	58.0	864 12	US-10-425-114-46828
13	2706.5	57.9	860 12	US-10-424-599-220216
14	2700.5	57.8	866 12	US-10-424-599-239573
15	2690	57.5	859 12	US-10-424-599-213159

16	2690	57.5	865 10	US-09-751-687-16	Sequence 16, Appl
17	2656.5	56.8	865 12	US-10-424-599-258944	Sequence 258944, A
18	2655.5	56.8	871 12	US-10-425-114-42385	Sequence 42385, A
19	2653	56.7	859 12	US-10-424-599-161981	Sequence 162981, A
20	2653	56.7	860 12	US-10-425-114-57755	Sequence 57755, A
21	2653	56.7	861 12	US-10-425-114-45728	Sequence 45728, A
22	2653	56.7	863 12	US-10-425-114-62362	Sequence 62362, A
23	2644.5	56.6	864 12	US-10-424-599-237909	Sequence 237909, A
24	2644.5	56.6	873 12	US-10-425-114-70099	Sequence 70099, A
25	2628.5	56.2	856 12	US-10-424-599-151513	Sequence 151513, A
26	2628.5	56.2	859 12	US-10-425-114-45902	Sequence 45902, A
27	2628.5	56.2	859 12	US-10-425-114-72413	Sequence 72413, A
28	2618	56.0	786 12	US-10-425-114-46295	Sequence 46295, A
29	2608.5	55.8	856 12	US-10-424-599-151512	Sequence 151512, A
30	2606	55.7	868 12	US-10-424-599-242598	Sequence 242598, A
31	2606	55.7	881 12	US-10-425-114-57754	Sequence 57754, A
32	2606	55.7	882 12	US-10-425-114-56555	Sequence 54555, A
33	2599	55.6	853 12	US-10-424-599-151510	Sequence 151510, A
34	2599	55.6	860 12	US-10-425-114-39867	Sequence 39867, A
35	2599	55.6	862 12	US-10-425-114-42418	Sequence 42418, A
36	2599	55.6	863 12	US-10-425-114-39883	Sequence 39883, A
37	2599	55.6	863 12	US-10-425-114-47348	Sequence 47348, A
38	2599	55.6	865 12	US-10-425-114-40151	Sequence 40151, A
39	2599	55.6	866 12	US-10-425-114-40047	Sequence 40047, A
40	2599	55.6	867 12	US-10-425-114-39889	Sequence 39889, A
41	2582.5	55.2	839 10	US-09-751-687-15	Sequence 15, Appl
42	2577.5	55.1	858 12	US-10-424-599-151515	Sequence 151515, A
43	2576	55.1	857 12	US-10-425-114-57794	Sequence 57794, A
44	2538.5	54.3	888 16	US-10-437-963-165232	Sequence 165232, A
45	2525	54.0	964 16	US-10-437-963-141895	Sequence 141895, A

ALIGNMENTS

RESULT 1
US-10-059-909-12

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; Sequence 12, Application US/10059909
; Publication No: US20030074693A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Kinney, Anthony
; APPLICANT: Klein, Theodore
; APPLICANT: Lee, Jian Ming
; APPLICANT: Pearlstein, Richard
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Shen, Jennie
; APPLICANT: Thorpe, Cathy
; APPLICANT: Tingey, Scott
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Lipoxigenases
; FILE REFERENCE: B01333 US CIP
; CURRENT APPLICATION NUMBER: US/10/059,909
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/501,422
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,597
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Momordica charantia
US-10-059-909-12
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Query Match 84.1%; Score 3933; DB 14; Length 880;
Best Local Similarity 81.7%; Pred. No. 0;
Matches 719; Conservative 83; Mismatches 76; Indels 2; Gaps 1;

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DB 1 MFGIGKNIIEGALNTGDLGSGVINAGGNIVRVTNIGGKIKGTIVLNRNVLDFTFPH 60

QY 61 SNLLDNFTLGGVSYFOLISATHSTNSDRSGVGNKAYLERWLTSIPLPAGESVFOINF 120
Db 61 SSLLDGVTELLGGISLQISATHASNSDRSGVGNKAYLERWLTSVPLPAGESVFOINF 120
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Db 121 DWENFGPGAPFIKNGHTSEFFLKSLLDLDVPGYGRVHFDNCNSWVPSGRYKDKRIPFA 180
QY 181 NHVLPSTQPNLRYRREELNWLGDGTGEKEWDRIVDYVDVNDIADPDVGH--RPI 238
Db 181 NHTCLPIDPDSLRKYREELNWLGDGTGEKEWDRIVDYVDVNDIADPDVGH--RPI 240
QY 239 LGGTEYPYPRGRGTRPRSRDRHNEYSRLSPINSLDIYVVKDENFGHKLMSDFLGYTLK 298
Db 241 LGGSQYQYPRGRGTRPRSRDRHNEYSRLSPINSLDIYVVKDENFGHKLMSDFLGYTLK 300
QY 299 ALSISIKPGLQSIQFVTPNEFDNFKEVDNLPERGPIPFNAFKLTEDLTPLPKALVRN 358
Db 301 VLSTIQPGLSIFDSTGEFDFKXEVDDLPERGPIPFNAFKLTEDLTPLPKALVRN 360
QY 359 DGEKTLKPTTPVWVNDKIGWSTDEFAFEMLAGNPILLIRLEAFPPSTSKLDPNVYGNQ 418
Db 361 DGERFLKPTTPVWVNDKIGWSTDEFAFEMLAGNPILLIRLEAFPPSTSKLDPNVYGNQ 420
QY 419 NSTITTEHKLHGLDGLTVDEAMKQNLRYIVDPHDALMPYLFRMATSKTATVATLILLK 478
Db 421 NSTITTEHKLHGLDGLTVDEAMKQNLRYIVDPHDALMPYLFRMATSKTATVATLILLK 480
QY 479 DGTTLKPLVIELALPHQDQDGLGALSILYFPAENGVOKSIWQAKAYVTVNDVGHOLIS 538
Db 481 DGTTLKPLVIELALPHQDQDGLGALSILYFPAENGVOKSIWQAKAYVTVNDVGHOLIS 540
QY 539 HMLTHAVLEPFIATHRQLSVLHPHKLHGLDGLTVDEAMKQNLRYIVDPHDALMPYLFRMATSKTATVATLILLK 598
Db 541 HMLTHAVLEPFIATHRQLSVLHPHKLHGLDGLTVDEAMKQNLRYIVDPHDALMPYLFRMATSKTATVATLILLK 600
QY 599 PSKYNESSILYKDWTPDQALPNNLMKRGGLAVEDSSAPHLRLINDYVPAVDGDIW 658
Db 601 PSKYNESSILYKDWTPDQALPNNLMKRGGLAVEDSSAPHLRLINDYVPAVDGDIW 660
QY 659 SAIKTWVQDCCLYKDDNAVQNDPELOSWMNELREKGHADKXGHEPWPQMOTSELIES 718
Db 661 SAIKTWVQDCCLYKDDNAVQNDPELOSWMNELREKGHADKXGHEPWPQMOTSELIES 720
QY 719 CTTIILWISSALHAANVFGQYPGYVILNRPPTTSRPFMEVGTAEYKELESNPEKAFURTI 778
Db 721 CTTIILWISSALHAANVFGQYPGYVILNRPPTTSRPFMEVGTAEYKELESNPEKAFURTI 780
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Db 781 SSOIALLGLSIIIEILSKHASDEVYLGORASIDWTSKIALEAFKFKGNLFVEVENRIME 840
QY 839 RNKENVNLKNSGPNVLPYTLVPSSNEGILTRGIPNSISI 878
Db 841 RNQDVLNLRAGPVNPNYTLVPSSNEGILTRGIPNSISI 880

RESULT 2

US-09-978-522-3
; Sequence 3, Application US/09978522
; Publication No. US2003003627A1
; GENERAL INFORMATION:
; APPLICANT: Descenzo, Richard
; APPLICANT: Irelan, Nancy
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
; FILE REFERENCE: 29520/37890
; CURRENT APPLICATION NUMBER: US/09/978,522
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,220
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Vitis LOX 2
US-09-978-522-3

Query Match 64.4%; Score 3011.5; DB 10; Length 859;
Best Local Similarity 64.9%; Pred. No. 3.5e-267;
Matches 547; Conservative 128; Mismatches 163; Indels 5; Gaps 3;

QY 41 KIKGKVIIMRSNVLDTEFEHNSLLDNFTLGGVSYFOLISATH--TSNDSRGKGNKAY 98
Db 17 KIKGTVLMKKNVLDNFNASVDRVHELLGQGVPLQLVSAVHGDPANGLOKIGKAY 76
QY 99 LERWLTSIPLPAGESVFOINFQWDBENFGGAFIKNKHTSEFFLKSITLDDVPGYGRV 158
Db 77 LEDMITITSLTAGESAFKVTDFDDEIGECAFIRNNHSEFYLRTLTLEDVPGRI 136
QY 159 HFDNCNSWVPSGRYKDKRIPFANHYLPSTQPNLRYRREELNWLGDGTGEKEWDRIV 218
Db 137 HFVCSNWVYPAQHYKTDVFTNQTLYPSETPGPLRYKREGELVNLRGDGTGELKEDRV 196
QY 219 YDVTVDNDIADP--DVGDHRPILGGTTEYPYPRGRGTRPRSRDRHNEYSRLSPIMSLDI 276
Db 197 YDVTVDNDIADP--DVGDHRPILGGTTEYPYPRGRGTRPRSRDRHNEYSRLSPIMSLDI 256
QY 277 YPKDENFGHKLMSDFLGYTLKALSISIKPGLQSIQFVTPNEFDNFKEVDNLPERGPIPF 336
Db 257 YPRDERFGLKMSDFLAYALKSIVQFLPEPEALCDITHNEFDFQDVLDIYEGGKVP 316
QY 337 FNAFKTLTLDLP--PLFKALVNDGEGKFLKRPTEPVWVNDKIGWSTDEFAFEMLAGNP 395
Db 317 EGPLDKIKDNIPLKMLKELVTDGHELFKPNQVQIKEDKSAWTKDEFAFEMLAGNP 376
QY 396 LIIRLEAFPPSTSKLDPNVYGNQNSTITTEHKLHGLDGLTVDEAMKQNLRYIVDPHDALM 455
Db 377 WIRLQEPFKSKLDPEVYGNQNSITKEIENHLLDITINEAMEKKRLFLDHDVFM 436
QY 456 PYLTRNATSTKYATRTLLKDDGTLPVIELALPHQDQDGLGALSILYFPAENGVO 515
Db 437 PYLTRNATSTKYATRTLLKDDGTLPVIELALPHQDQDGLGALSILYFPAENGVO 496
QY 516 KSIWQAKAYVTVNDVGHQLISHLHTHAVLEPFIATHRQLSVLHPHKLHGLDGLTVDEAM 575
Db 497 GSIWQAKAYVTVNDVGHQLISHLHTHAVLEPFIATHRQLSVLHPHKLHGLDGLTVDEAM 556
QY 576 MFINASARQVLINAGLIETTHYPSKYSMELSSILYKDWTPDQALPNNLMKRGGLAVEDS 635
Db 557 MFINASARQVLINAGLIETTHYPSKYSMELSSILYKDWTPDQALPNNLMKRGGLAVEDS 616
QY 636 SAPHGLRLINDYVPAVDGLDIWSAICTWQYCCLYKDDNAVQNDPELOSWMNELREK 695
Db 617 EAPHGLRLINDYVPAVDGLDIWSAICTWQYCCLYKDDNAVQNDPELOSWMNELREK 676
QY 696 GHADKXGHEPWPQMOTSELIESCTTIILWISSALHAANVFGQYPGYVILNRPPTTSRPF 755
Db 677 GHADKXGHEPWPQMOTSELIESCTTIILWISSALHAANVFGQYPGYVILNRPPTTSRPF 736
QY 756 PEVGTAEYKELESNPEKAFURTI CSELOALVSIIEILSKHASDEVYLGORASIDWTS 815
Db 737 PEVGTAEYKELESNPEKAFURTI CSELOALVSIIEILSKHASDEVYLGORASIDWTS 796
QY 816 KIALEAFKFKGNLFVEVENRIME RNKENVNLKNSGPNVLPYTLVPSSNEGILTRGIPNS 875
Db 797 TTPKAFKXGHEPWPQMOTSELIESCTTIILWISSALHAANVFGQYPGYVILNRPPTTSRPF 856
QY 876 ISI 878
Db 857 VSI 859

RESULT 3

US-09-978-522-1

Sequence 1, Application US/09978522
Publication No. US20030033627A1
GENERAL INFORMATION:
APPLICANT: Descenzo, Richard
APPLICANT: Ireland, Nancy
TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
FILE REFERENCE: 29520/37890
CURRENT APPLICATION NUMBER: US/09/978,522
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,220
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent version 3.0
SEQ ID NO 1
LENGTH: 862
TYPE: PRT
ORGANISM: Vitis LOX 1
US-09-978-522-1

Query Match 64.1%; Score 2995.5; DB 10; Length 862;
Best Local Similarity 63.6%; Pred. No. 1e-265;
Matches 546; Conservative 134; Mismatches 169; Indels 9; Gaps 4;

QY 30 ILDRVSSIGG---NKIKGKVLKMSNVLDPTEPHSNLDNFTTELLGGVSPQLISATH- 84
DB 5 LLSIVSAITGENDKKKIEGTIVLMKNVLDNFNAPVRDRVHFLFGQVSLQLVSAVG 64
QY 85 -TSNDSRGKVGKAYLERWLTSPPLFAGSVFQINFQWDFNFGFPFGAFIKNGHTSEFF 143
DB 65 DPANGLOKGLKPAYLEDWITITSLTAGSAFAKVTVDWEIGECPGAFIRNNHSEFY 124
QY 144 LKSLTLDVPGYGRVHPCNSWVYPSGKDYKDRIFFAHNVYLPSCNPNPLKRYREELWN 203
DB 125 LRTLTLEDVPGRIHFCVNSWVYPAKHKTDRVFFNTQTYLPSETPGPLRKYRKGELVN 184
QY 204 LRGGTGERKEDWRIYDNDIADP--DVGDHRPILGGTTEYPPRRGRTGRPRRRD 261
DB 195 LRGGTGBELKEDWVDVAYVNDLCKPDRDLKYARPVLGSAEYPPRRGRTGRPPSEKD 244
QY 262 HNYESRLSPIMSLDIYVPKDNFQHLKMSDFLGLTYLKALSISIKPGIQSIFDVTVPNFDN 321
DB 245 PKTESRLPLVMSLNIYPRDRFQHLKMSDFLAYALKSIYQFLPPEALCDITPNEFDS 304
QY 322 FKEVDNLPERGFPPIPENAFKTLTDLTP-PULFALVNDGDKFLKFFTPPEVVDKNKIGWS 380
DB 305 FQVDLDLYEGGIKYPEGELLDKIDNIPLEMLKELVRTDGBHLKFPMPQVVKEDKSAWR 364
QY 381 TDESFARMLAGPNPLLRLEAPPTSKLPDPNVYGNQNSITTEHIXHGLDGLTVDEAM 440
DB 365 TDESFARMLAGPNVIRLLQEPFPPKSKLPDPVYGNQNSITKEHIENHLDDLTINEAM 424
QY 441 KQNRLYIVDFHDLAMPYLTRNATSTKYATRTLLLLKDDGLTKPLVIELALPHEQDQL 500
DB 425 EKRLFLDHDVDFMYPURINTSTKYASRTLLFLKDDGLTKPLVIELALPHEQDGF 484
QY 501 GAISKLYPEAENGVOKSIWQLAKAYVTVNDVGYHQLISHWLHNAVLEPFIATHRLSV 560
DB 485 GAVNKVYTPAEDGVEGSIWQLAKAYAAVNDVGYHQLISHWLHNAVLEPFIATHRLSV 544
QY 561 LHPHKLIVPHKYOTMFINASARQVLINAGLIETTHYPKSKSMELSSILYKDWTFPDQA 620
DB 545 LHPHKLIVPHFRDFTMN:NALARQILINAGGVSTVFPFSKYAMEMSVVYKDWLVEQA 604
QY 621 LPNMLKGLAVEDSSAPHLRLINDYPPFADGLDITWSAIKTWVQDYCCLYKDDNAVQ 680
DB 605 LPADLILKGMAVEDSEAPHLRLINDYPPFADGLDITWSALETWVKEYCSFYKTDWVQ 664
QY 681 NDFELQSWNELREKGHADKHPWPKQTLSELIBSCCTIIWIASALHAANVFGQY 740
DB 665 KDSELSQSWKEVREHGHGDKDEPWPWPKQRTVKELIETCTIIWVASALHAANVFGQY 724
QY 741 GGYILNRPITSRPFMEPTGTEYBELKGNPKDAFLKTITTAQLQTLIGISLIEVLGRHSD 784

QY 801 EYVIGORASIDWTSKIALAEAFKGNLFVENRIMERNKEVNILKNSRGPVNLPTLLV 860
DB 785 EYVIGORDTPWILDTTPLKAFKGRKLADIEEMIIDRNGNERFNVRGVPKIPITLLY 844
QY 861 PSNEGLTGCGIPNSISI 878
DB 845 PTSEGLTGKGPNSVSI 862

RESULT 4
US-10-425-114-54449
Sequence 54449, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54449
LENGTH: 887
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701209742_FLI.pep
US-10-425-114-54449

Query Match 62.7%; Score 2929; DB 12; Length 887;
Best Local Similarity 61.1%; Pred. No. 1.4e-259;
Matches 527; Conservative 141; Mismatches 182; Indels 12; Gaps 3;

QY 29 NILDRVSSIG------GNKIKGVILKMSNVLDPTEPHSNLDNFTTELLGGVSPQLISA 82
DB 26 NIMNAPTTTGGDNDGPHRVKGTIVLMKNVLDNFDFGASFLDLRHEFVGVKSVLQVSS 85
QY 83 TH----TSNDSRGKVGKAYLERWLTSPPLFAGSVFQINFQWDFNFGFPFGAFIKNGH 138
DB 86 VNVDPGNGLKGKLPAYLEDWITITSLTAGSAFAKVTFEDEEIGTPGAFIRNNH 145
QY 139 TSEFFFLKSLTLDVPGYGRVHPCNSWVYPSGKDYKDRIFFAHNVYLPSCNPNPLKRYRE 198
DB 146 HSEFYLKSLTLEDVPGQGVIRFCNSWVYPADKYEKDRIFPNSKTYLPSETMPLLYKRE 205
QY 199 BELWNLRGDTGERKEDWRIYDNDIADPVDGH--RPILGGTTEYPPRRGRTGRP 256
DB 206 ELENLRGNGKQQLQEDWDRVYDLYALDNGNPKDPQHARPLTGGSKDYPPRRGRTSRP 265
QY 257 RRRRDHNYESRLSPIMSLDIYVPKDNFQHLKMSDFLGLTYLKALSISIKPGIQSIFDVTVP 316
DB 266 PAKSDPKCSRLNIASSLDIYVPRDERFQHLKMAADFALVALKSIYQVLKPEFESLFDSTP 325
QY 317 NEFDNPKVDNLPFERGFPPIFNAFKTLTDLTPPLFALVNDGDKFLKFPPEVVDKNK 376
DB 326 NEFDKPEDVLKLYEGIEVPEGILTVEVRDNIPEALMKEIFRSDGQRLKLPFPQVIADV 385
QY 377 IGWSTDEEFARMLAGPNPLLRLEAPPTSKLPDPNVYGNQNSITTEHIXHGLDGLTV 436
DB 386 SAWQDDEFGRELLAGINVFVIRGQEPFPAKLPDPKIYGNQTSITKEHIESNLEGFV 445
QY 437 DEAMKQNRLYIVDFHDLAMPYLTRNATSTKYATRTLLLLKDDGLTKPLVIELALPHEQ 496
DB 446 DEAIKERRLLPILDLHALIPYKVRINSTSTKMYASRTILFLQDSGTLKPLALIELSLPHE 505
QY 497 GDQLGAISKLYPAENGVOKSIWQLAKAYVTVNDVGYHQLISHWLHNAVLEPFIATHR 556

Db 506 GQOYGAISKVYTPVBOG:ENSWQLAKAYVVVDSGYHQLISHWLHHAHVEIPILATNR 565
QY 557 QLSVLHPHKLIVPHYKDTMTFNASAROVLINANGLIETTHYPKYSNELSSILYKDWTF 616
Db 566 HUSVLHPHKLIVPHYKDTMTFNALGRQILINAGALELTVCPKYSNEFSSVLYKDWVF 625
QY 617 PDQALPNMLKRGGLAVEDSSAPHGLLELLINDYPFAVDGLDIWSAIKTWODYCCLYKDD 676
Db 626 PEQALPEDLVKRGVAVKDSSTPYGLRLIEDYPFAVDGLLEIWPALKTWKDYCSFYKED 685
QY 677 NAVQNDPELOSWNELREKHKHAKHEPWPWPKMOTLSBELISCTTIWIASALHAANFG 736
Db 686 DTYKDDTSLQSWKEIREVGHGDKDEPWPWPKMOTLSBELISCTTIWIASALHAANFG 745
QY 737 QYPYGGYILNRPTTSRRPMPVGTAEYKELESNPEKAFPLRTICSELOALVSIIEILSK 796
Db 746 QYPYGGFPSPRPAISRRPMPKGTPEYDELVANPKAYLKVTSQFLAVLGISLVEILSK 805
QY 797 HASDEVYLGQASIDWTSKIALEAFKFGKNLFEVENRINERKNVNLKNSGPNLPY 856
Db 806 HSSDEVYLGQRTDPDWTSDABPQAFKFGKGLADIBERILMNSDEKFRNRYGPNVMPY 865
QY 857 TLLVPSSNEGLTGRGIPNSISI 878
Db 866 TLLYFSSKGLTGMGVFNSISI 887

RESULT 5
US-10-424-599-215976
; Sequence 215976, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215976
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37056C.1.pap
US-10-424-599-215976

Query Match 59.8%; Score 2795; DB 12; Length 857;
Best Local Similarity 60.4%; Pred. No. 2.9e-247;
Matches 525; Conservative 131; Mismatches 181; Indels 32; Gaps 7;
QY 28 GNILDRVSSLOGNKIKGVILMRNSVLDFTBFHS-----NLLDNFTFELGGG 74
Db 3 GCLLHR-----GHKIKGTWLMRKNVLDVNSVTSVGGIIGQLDLVAGSTLDTLTAFLGRS 57
QY 75 VSFOLISATHTSNDRSGVGNKAVLERWLTSTIPPLFAGESVFQINFOWDENFGPPGAFFI 134
Db 58 VSLQISATKADANGKGLKATLEGITISLPTLGAGQSAFKINFEDDGGSGIPGAFYI 117
QY 135 KNIGHTSEFFLSLTLDDVPYGRVHFCNCSWVYPSGRYKDKRIFPANHVLPSQTNPLR 194
Db 118 KNFMQTEFFLSLTLDEDIPNEGSIHFVCSWYNAKLFKSDRIFFANQTVLPSETPAVLV 177
QY 195 KYREELNLRGDCGKERKENDRYDYVDYNDIADPDVGDH--RPILGCTTEYPYRGR 252
Db 178 KYREELNLRGDCGKERKENDRYDYVDYNDIADPDVGDH--RPILGCTTEYPYRGR 237
QY 253 TGRPRSRDRHYEKLSPMSLDIYVPKDNENFGLHKNMSDFLGYTLKALISISIKPGLQSI 312

Db 238 TGRKPTRKDPNSES-----SNDVYLPRDEAFGLHKSDFLTLYGLKSVSNVLPLOQSAF 292
QY 313 DV--TPNEBDFNPFVDNLPFERGFPIPPNFAFKTLTLEDLP-PLFKALVNDGCEKFLKPTTP 369
Db 293 DLNFTPREDSFDEVHGLYGGIKLPTD-----ITSKISPLVLKEIFTDGEQALKFPPP 348
QY 370 EYVKONKIGWSTDEEFAREMLAGPNPLIRLEAPFPPTSCLDPNPNYGNQNTTITEEHK 429
Db 349 KVIQVSKSAMWTDSEFAREMLAGVNPILRCIKDPFPRSKLDSQVYGDHSTQITKEHLEP 408
QY 430 GUDGLTVDKAMKONELYIVDPHDALMPYLTRNATSTKYATRTLLLLKDKGTLPKPIVE 489
Db 409 NLEGLTVDKAIQNKRLFLDDHDPIMPYLRRLNATSTKAYATRTLLFKNDGTLPKPIVE 468
QY 490 LALPFPQDQLGAIKSLYFPAENGVCQSIQWOLAKAYVTVNDVYHQLISHWLHHAHVEIP 549
Db 469 LSLPFPQDQSGAFSQVFLPADGEGVESIWLAKAYVVVNDSCYHQLVSHMLNTHAVVEP 528
QY 550 FVIAHROQLSVLHPHKLIVPHYKDTMTFNASAROVLINANGLIETTHYPKYSNELSSI 609
Db 529 FIATNRHLSVVPHTYKLLHPHYRTMNINGLARLSLVNDGCVTEQTLWGRYSVMSAV 588
QY 610 LYKQMTFPDQALPNMLKRGGLAVEDSSAPHGLRLLEINDYPFAVDGLDIWSAIAIKTWODYC 669
Db 589 VYKDWVFTDQALPADLKEGMAIEDPSCPHGLRLVIEDYPFAVDGLEIWDALKTWVHYV 648
QY 670 CLYKDDNAVQNDPELOSWNELREKHKHAKHEPWPWPKMOTLSBELISCTTIWIASAL 729
Db 649 FLYKSDDTLREDPELOQWELVEVGHGDKNEPWPWPKMOTREBELVEACAIITWASAL 708
QY 730 HAAVNFQYPGYILNRPTTSRRPMPVGTAEYKELESNPEKAFPLRTICSELOALVSI 789
Db 709 HAAVNFQYPGYILNRPTTSRRPMPVGTAEYKELESNPEKAFPLRTICSELOALVSI 768
QY 790 IIEILSKHSDDEVYLGQASIDWTSKIALEAFKFGKNLFEVENRINERKNVNLKNS 849
Db 769 VIEILSRHSDDEVYLGGERDNPWTSDTRALEAFKFGKNLAQIENKLSERNNDEKLNR 828
QY 850 GPVNLPTLLVPSSNEGLTGRGIPNSISI 878
Db 829 GPVQMPYTLTLLPSKEGLTFRGIPNSISI 857

RESULT 6
US-10-425-114-45769
; Sequence 45769, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45769
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700675903_FLI.pap
US-10-425-114-45769

Query Match 59.8%; Score 2795; DB 12; Length 860;
Best Local Similarity 60.4%; Pred. No. 2.9e-247;
Matches 525; Conservative 131; Mismatches 181; Indels 32; Gaps 7;
QY 28 GNILDRVSSLOGNKIKGVILMRNSVLDFTBFHS-----NLLDNFTFELGGG 74


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Db 6 GGLLHR-----CHKIKGTWLMKKNVLDVNSVTVGGIIGQGLDLVGSTLDTLTAFIAGRS 60
Qy 75 VSFQIISATHTSNDSRGKVGKAYLERWLTSIPPLFAGESVQFQINQFOWDENFGPPGAFPI 134
Db 61 VSLQIISATKADANGKGLKATFLEGIITSPLTLGAGQSAFKINFEDWDGSGIPGAFYI 120
Qy 135 KNIGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWYPSGRYKKDRIFFAHVHVLPSQTPNPLR 194
Db 121 KNFMQTEFFLVSLTLEDIPNHGSIHFVCSNWIYNAKLFKSDRIFFANQTYLPSETAPLV 180
Qy 195 KYREELNWLNGDGTGERKEWDRIDYDVNDIADPDVGDH--RPILGGTTEYPYPRGR 252
Db 181 KYREELNWLNGDGTGERKEWRIYDYVDYNDLGDGPKGENHARVPLGGNDTTFYPRGR 240
Qy 253 TGRPSRRDHNYESRLSPIMSLDIYVPKDNFGLHKKMSDFLGYTLKALSISIKPGLQSI 312
Db 241 TGRKPTRKDPSSESR-----SNDVYLPKDEAFGLKSSDFLTGLKSVSNVLPQLQSAF 295
Qy 313 DV--TPNEFDNFKEVDNLFERGFPIPFNAFKTLTLEDLTP-PLFKALVRNDGKFLKFPPT 369
Db 296 DLNFTPREFDSFDEHGLYSGGIKLPD-----IISKISPLPVKBEIFRTDGEQALKFPPP 351
Qy 370 EWDKNGKIGWSTDEEFAREMLAGNPLLIIRLEAFPPPTSKLDPNVYGNQNSTITEBIKH 429
Db 352 KVIQVKSANWMTDEEFAREMLAGVNPNIIRCLKDFPRSKLDQVYGDHTSQITKEHLEP 411
Qy 430 GLDGLTVDEAMKQNLVIYDFHDLAMPYLTRNATSTKYATRTLLLLKDDGLTKPLVIE 489
Db 412 NLEGLTVDEAIQNKLFLLDHDHPIMPYLRINATSTKAYATRTILFLKNDGTLRPLAIE 471
Qy 490 LALPHQDQDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGVHQLISHMLHTHAVLEP 549
Db 472 LSLPHQDQSGAFSQVFLPADEGVESIWLLAKAYVVVNDSCVHQVLSVHMLTHAVLEP 531
Qy 550 FVIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIETHTHPSKYSMELSSI 609
Db 532 FIATNRHLSVVHPHYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTLFGLWGRYSVMSAV 591
Qy 610 LYKDWTFDQALPNNLMKRGVAVDSAPHLRLILINDYPAVDGLDLSAIKTTWQDYC 669
Db 592 VYKDWVTFDQALPADLIRKGMALIEDPSCPHGIRLVIEDYPAVDGLDLSAIKTTWQDYC 651
Qy 670 CLYKDWTFDQALPADLIRKGMALIEDPSCPHGIRLVIEDYPAVDGLDLSAIKTTWQDYC 729
Db 652 FLXYKSDDTLREDPDLQACWKELVGCHGDKKNEPWPWKQTRLEAVEACAIITWASAL 711
Qy 730 HAAVNFQGYPYGGYILNRPPTSRFPMPVEVGTAEYKELESNPEKAFLETICSELOALVSI 789
Db 712 HAAVNFQGYPYGGYILNRPPTSRFPMPVEVGTAEYKELESNPEKAFLETICSELOALVSI 771
Qy 790 IIEILSKHASDEVYLGORASIDWTSKIALEAFKFGKNIPEVENRIMERNKEVNLKRS 849
Db 772 VIEILSRHASDEVYLGORASIDWTSKIALEAFKFGKNIPEVENRIMERNKEVNLKRS 831
Qy 850 GPVNLPTYLLVPSSNEGLTGRGIPNSISI 878
Db 832 GPVQMPYTLPLPSKKEGLTFRGIPNSISI 860
```

RESULT 7

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US-10-425-114-54429
; Sequence 54429, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54429
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700842448_FLI.pep
US-10-425-114-54429
```

Query Match 59.8%; Score 2795; DB 12; Length 863;

Best Local Similarity 60.4%; Pred. No. 2.9e-24;

Matches 525; Conservative 131; Mismatches 181; Indels 32; Gaps 7;

```
Qy 28 GNILDRVSLGNGKIKGKIVLMRSNVLDPTBFHS-----NLLDNFTLLGGG 74
Db 9 GGLLHR-----CHKIKGTWLMKKNVLDVNSVTVGGIIGQGLDLVGSTLDTLTAFIAGRS 63
Qy 75 VSFQIISATHTSNDSRGKVGKAYLERWLTSIPPLFAGESVQFQINQFOWDENFGPPGAFPI 134
Db 64 VSLQIISATKADANGKGLKATFLEGIITSPLTLGAGQSAFKINFEDWDGSGIPGAFYI 123
Qy 135 KNIGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWYPSGRYKKDRIFFAHVHVLPSQTPNPLR 194
Db 124 KNFMQTEFFLVSLTLEDIPNHGSIHFVCSNWIYNAKLFKSDRIFFANQTYLPSETAPLV 183
Qy 195 KYREELNWLNGDGTGERKEWDRIDYDVNDIADPDVGDH--RPILGGTTEYPYPRGR 252
Db 184 KYREELNWLNGDGTGERKEWRIYDYVDYNDLGDGPKGENHARVPLGGNDTTFYPRGR 243
Qy 253 TGRPSRRDHNYESRLSPIMSLDIYVPKDNFGLHKKMSDFLGYTLKALSISIKPGLQSI 312
Db 244 TGRKPTRKDPSSESR-----SNDVYLPKDEAFGLKSSDFLTGLKSVSNVLPQLQSAF 298
Qy 313 DV--TPNEFDNFKEVDNLFERGFPIPFNAFKTLTLEDLTP-PLFKALVRNDGKFLKFPPT 369
Db 299 DLNFTPREFDSFDEHGLYSGGIKLPD-----IISKISPLPVKBEIFRTDGEQALKFPPP 354
Qy 370 EWDKNGKIGWSTDEEFAREMLAGNPLLIIRLEAFPPPTSKLDPNVYGNQNSTITEBIKH 429
Db 355 KVIQVKSANWMTDEEFAREMLAGVNPNIIRCLKDFPRSKLDQVYGDHTSQITKEHLEP 414
Qy 430 GLDGLTVDEAMKQNLVIYDFHDLAMPYLTRNATSTKYATRTLLLLKDDGLTKPLVIE 489
Db 415 NLEGLTVDEAIQNKLFLLDHDHPIMPYLRINATSTKAYATRTILFLKNDGTLRPLAIE 474
Qy 490 LALPHQDQDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGVHQLISHMLHTHAVLEP 549
Db 475 LSLPHQDQSGAFSQVFLPADEGVESIWLLAKAYVVVNDSCVHQVLSVHMLTHAVLEP 534
Qy 550 FVIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIETHTHPSKYSMELSSI 609
Db 535 FIATNRHLSVVHPHYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTLFGLWGRYSVMSAV 594
Qy 610 LYKDWTFDQALPNNLMKRGVAVDSAPHLRLILINDYPAVDGLDLSAIKTTWQDYC 669
Db 595 VYKDWVTFDQALPADLIRKGMALIEDPSCPHGIRLVIEDYPAVDGLDLSAIKTTWQDYC 654
Qy 670 CLYKDWTFDQALPADLIRKGMALIEDPSCPHGIRLVIEDYPAVDGLDLSAIKTTWQDYC 729
Db 655 FLXYKSDDTLREDPDLQACWKELVGCHGDKKNEPWPWKQTRLEAVEACAIITWASAL 714
Qy 730 HAAVNFQGYPYGGYILNRPPTSRFPMPVEVGTAEYKELESNPEKAFLETICSELOALVSI 789
Db 715 HAAVNFQGYPYGGYILNRPPTSRFPMPVEVGTAEYKELESNPEKAFLETICSELOALVSI 774
Qy 790 IIEILSKHASDEVYLGORASIDWTSKIALEAFKFGKNIPEVENRIMERNKEVNLKRS 849
Db 775 VIEILSRHASDEVYLGORASIDWTSKIALEAFKFGKNIPEVENRIMERNKEVNLKRS 834
Qy 850 GPVNLPTYLLVPSSNEGLTGRGIPNSISI 878
```


Db 349 KVIQVSKSAWMTDEPAREMLAGVNPILRLCKDPFRPSKLDQVGDHTSQITKEHLEP 408
Qy 430 GLDGLTVDEAMKQNRILVIVPHDMLPILTRMNAATSTKATYATRLLLKDDGTLKPLVIE 489
Db 409 NLEGLTVDEATQNRLLFLDHDHPIMPYLRINATSTKAYATRTILFLKNDGTLPLAIE 468
Qy 490 LALPHQDQDGLGALSILYFPAENGVOKSIWOLAKAYTVNDVGVHQLISHWLTHAVLEP 549
Db 469 LSLPHQDQDQSGAFSQFLPADEGVSSIWOLAKAYTVNDVGVHQLISHWLTHAVLEP 528
Qy 550 FVIATHRQLSVLPHILKLLVPHYDXTMFINASARQVLINANGLIETTHYPSKYSMELSSI 609
Db 529 FIATNRHLSVVHPIYKLLPHYRDTWNINGLARSLVNDGVIEQTFFLMGYSVMSAV 588
Qy 610 LYKDWTPDQALPNNLMKRGIAVEDSSAPHCLRLILINDYFPAVDGLDINSAIKTWQDYC 669
Db 589 VYKDWTFDQALPADLIRGMAIEDPSPCHGIRLVIEDYPTVVDGLSEIWDIAIKTWVHEVY 648
Qy 670 CLYTKDDNAVONDFELQSWNNELREKHAADKHPMPKMQTSLSELIESCTTIITWIASAL 729
Db 649 FLYYKSDTLREDPELOACWKELVEVGHGDKNEPMPKMQTRELVEACAILIWTASAL 708
Qy 730 HAAVNFQGYPGGILNRPTRSPMPVEVGTAEYKELESNPEKAFPLATICSERQALVSIIS 789
Db 709 HAAVNFQGYPGGILNRPTRSPMPVEVGTAEYKELESNPEKAFPLATICSERQALVSIIS 768
Qy 790 IIEILSKHASDEVYLGORASIDWTSKIALEAFKFKNLFVENRIMERKNEVNLKNS 849
Db 769 VIEILSRHASDEVYGERDNPNTSDTRALEAFKFKNLAQENKLSERNDEKLENRC 828
Qy 850 GPVNLPTLLVPSNEGTLRGIPNSISI 878
Db 829 GPVQMPYTLPLPSKKEGLTRGIPNSISI 857

RESULT 10

US-10-424-599-215973
; Sequence 215973, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215973
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37053C.1.pep
US-10-424-599-215973

Query Match 58.7%; Score 2742.5; DB 12; Length 826;
Best Local Similarity 60.2%; Pred. No. 1.8e-242;
Matches 515; Conservative 135; Mismatches 169; Indels 37; Gaps 9;

Qy 28 GNILDRVSSLGKNTKGVILMRSNVLDFTFEHNLNDNTELLGGGVSQLISATHSN 87
Db 3 GGLIHR-----GHKIKGVILMRKNVLD-----VNSVTSV--GGIIQQA----- 39
Qy 88 DSRGKGVNKAYLERWLTSIPPLFAGESVQINFQWENFGFPAGFAFFKNGHTEFFLKSL 147
Db 40 NGKGLGKATLEGIITSLPLTGAGQSAFKINFEDDGGIPGAFYIKNFQTEFFLVSL 99
Qy 148 TLDDVPGVGRVHFCNWSWVPSGKYKDRIPFAHNVLPQTPNPLKRYEBELNLNRGD 207
Db 100 TLEDIPNHGSHFVCSNWIYNAKLKFDRIFFANQYLPSETPAPLVKYREBELNLNRGD 159

Qy 208 GTGERKEWDRIVDYVYNDIADDPVGDH--APILGGTTEYPYPRRGRTGRPSRRDHNYE 265
Db 160 GTGERKEWERIYDYVYNDLGDGDPKGENHARFVLGNDTFYPRRGRTGRKPTRKDPNSE 219
Qy 266 SLSLSPIMSLDIYVPKDENFHGLKMSDFLGTYTLKALSISIKPGLOQSIQFV--TPNEFDNFK 323
Db 220 SR-----SNDVYLPDEAFHGLKSSDFLTGKLSVQNVLPQLQSAFADLNTTFREDFSD 274
Qy 324 EVDNLFERGFPIPFNAFKTLTDELTP-PLFKALVRNDGEKFLKPTTPEVVKDKIGWSTD 382
Db 275 EYHGLYSGIKLPTD-----IISKISFLPVLKEIFRTDGEQALKFPFPKVIQVSKSAMWTD 330
Qy 383 BEFAREMLAGNPLILRLEAPPTSKLDPNVGNQNSTITEEHKHLGDLGTVDEAMKQ 442
Db 331 BEFAREMLAGVNPILRLCKEFPFRSKLDSQVIGDHTSQITKEHLEPNLEGLTVDEALQN 390
Qy 443 NELYIVDFHDALPMLYTRMNAATSTKYATRTLLKDDGTLKPLVIELALPHPOQDQJGA 502
Db 391 KELFLDHDHPIMPYLRINATSTKAYATRTILFLKNDGTLRLPLAIELSLPHPOQDQSGA 450
Qy 503 ISKLYFPAENGVOKSIWOLAKAYTVNDVGVHQLISHWLTHAVLEPFIATHRQLSVLH 562
Db 451 FSQVFLPADEGVSESIWLLAKAYVVVNDSCYHQLVSHWLTHAVVEPFIATNRHLSVVH 510
Qy 563 PIHKLLVPHYKDTMTFINASARQVLINANGLIETTHYPSKYSMELSSILYKDWTFDQALP 622
Db 511 PIYKLLPHYRDTWNINGLARSLVNDGVIEQTFWGRYSVMSAVYKDWVTFDQALP 570
Qy 623 NNMKRGIAVEDSSAPHGLRLILINDYFPAVDGLDINSAIKTWQDYCCLYKDDNAVOND 682
Db 571 ADLIRGMAIEDPSPCHGIRLVIEDYPTVYAVDGLSEIWDIAIKTWVHEVYFLYKSDTLRED 630
Qy 683 FELQSWNNELREKHAADKHPMPKMQTSLSELIESCTTIITWIASALAAVNFQGYPGG 742
Db 631 PELQACWKELVEVGHGDKNEPMPKMQTRELVEACAILIWTASALAAVNFQGYPGG 690
Qy 743 YILNRPTRSPMPVEVGTAEYKELESNPEKAFPLRTICSELOALVSIISIEILSKHASDEV 802
Db 691 LILNRPTRSPMPVEVGTAEYKELESNPEKAFPLRTICSELOALVSIISIEILSKHASDEV 750
Qy 803 YLGORASIDWTSKIALEAFKFKNLFVENRIMERKNEVNLKNSRGPVNLPTLLVPS 862
Db 751 YLGERDNPNTSDTRALEAFKFKNLAQENKLSERNDEKLENRCRCPVQMPYTLPLPS 810
RESULT 11
US-10-425-114-45631
; Sequence 45631, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jiaodong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45631
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700733503_FLI.pep

US-10-425-114-45631

Query Match 58.7%; Score 2742.5; DB 12; Length 832;
Best Local Similarity 60.2%; Pred. No. 1.8e-242;
Matches 515; Conservative 135; Mismatches 169; Indels 37; Gaps 9;

QY 28 GNILDRVSSLGNGKIKGVILMRSNVLDFTFHHNLDNFTFELGGVSPQLISAHTSN 87
DB 9 GOLLER-----GHKIKGVILMRKNVLD-----VNSVTSV--GGIIQGA----- 45

QY 88 DSRGVGNKAYLERLWLTIPPLFAGESVQINFDENFGPGGAFFIKNGHTSEFFLKSL 147
DB 46 NGKGLKGRATFLEGIITSLPLGAGSAFKINFENDDGSGIPGAFYIKNFMQTEFFLVSL 105

QY 148 TLDDVPGVGRVHFDGNSWYPSGRYKDRIFPANHVLPSQTPNPLRKYEELLWNLRGD 207
DB 106 TLEDIPNHSIHFCVNSIYNKLFKSDRIFFANQTYLPSETPAPLVKYREEELHNLRGD 165

QY 208 GTGERKEWDRIVDYVDNDIADPDVGDH--RPILGGTTEVPYPRGRGTRPRRRDHYE 265
DB 166 GTGERKEWERYDYVDNDLGDGPKGENHARPVLGGNDTFYPRGRGTGRKTRKDPNSE 225

QY 266 SRLSPIMSLDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLQSIQFV--TPNEFDNFK 323
DB 226 SR-----SNDVYLPRDEAFGLKSDSLTYGLKSVSQNVLPPLQSAFDLNFTRPFDSPD 280

QY 324 EVDNLFEFGFPIPNNAFTLTEDLTP-PLFKALVRNDGKFLKEPTPEVVKDKNGIWSHD 382
DB 281 EVHGLYGGIKLPTD-----IISKISPLGVPVLKEIFRTDGEQALKEPPPKVQVSKSAMTD 336

QY 383 BEFAREMLAGNPLLRLEAPPTSKLDPNVYGNQNSTITEEHIKGLDGLTVDEAMKQ 442
DB 337 BEFAREMLAGNPNLRCLKEFPFRSKLDSQVYGDHTSQITKEHLEPNLGLTVDEAIQN 396

QY 443 NRLIYVDPHDMPLFMNATSTKYATRTLLLLKDDGLTKPLVIELALPHQDGLGA 502
DB 397 KRLFLDHDHDPIMPLRRLNATSTKAYATRTILFLKNDGTLRPLAIELSLPHQDQSGA 456

QY 503 ISKLYFPAENGQKSIWOLAKAYTVNDVGHQILSHLHHAVALPEPFIATNRHLSVH 562
DB 457 FSQVPLPADEGVESILWAKAYVNDVSCYHQLVSHLWNTHAVVEPFIATNRHLSVH 516

QY 563 PIHKLVLPHYKDTFTINASARQVLINANGLIETTHYPSKYSMELSSILYKDWTFDQALP 622
DB 517 PIYKLLPHYDRTWNINGLARLSLVNDGGVTEQTFWGRYSKVSMSAVVYKDWTFDQALP 576

QY 623 NNLKRGGLAVSDSAPHLRLINDYPAVDGLDIWSAIKTWQDYCCLYKDDNAVOND 682
DB 577 ADLIRKGNALIEDPSPCHGIRLVIEDYPAVDGLDIWDAIKTWVHYVLYKSDDTLRED 636

QY 683 FELQSWNELREKGHADKKHPPWPKMQTSELIESCTTIITWASALHAAVNFQPYGG 742
DB 637 PELQACWELVEVGHGDKNEPWPQMQTRELVEACAIITWASALHAAVNFQPYGG 696

QY 743 YILNRPTTSRPMPEBVGTAEYKELSPKAFLETICSELOALVSIIEILSKHASDEV 802
DB 697 LILNRPTLSRPMPEKSAEYELRKNPQKAYLTIITPKFTLIDLVSIELSRHASDEV 756

QY 803 YLGRASIDWTSKIALEAFKFGKNIPEVENRIMERNEKYNLKRSGPNLYTYLLVPS 862
DB 757 YLGERDNPWTSIDTRALEAFKFGKNIPEVENRIMERNEKYNLKRSGPNLYTYLLVPS 816

QY 863 SNEGLTGRIENSTSI 878
DB 817 SREGLTFRGIENSTSI 832

RESULT 12

US-10-425-114-46828
; Sequence 46828, Application US/10425114
; Publication No. US20040034898A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 46828
LENGTH: 864
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701040644_FLI.pap
US-10-425-114-46828

Query Match 58.0%; Score 2713.5; DB 12; Length 864;

Best Local Similarity 57.3%; Pred. No. 9.1e-240;

Matches 497; Conservative 166; Mismatches 185; Indels 19; Gaps 11;

QY 23 VINAGGNILDRVSSLGNGKIKGVILMRSNVLDFTFHHNLDNFTFELGGVSPQLISA 82
DB 6 INEVANQIVER-----SKRVKGRVVMKGVLDFFEDIKANVLDRVHLLGKGVSLQLISA 60

QY 83 THTSNDSRGKV-GNKAYLERWLTSTIPPLFA-GESVQINFDENFGPGGAFFIKNGHTS 140
DB 61 T-TPPAKGLLRGKGVANLERWVTSITSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 119

QY 141 EFELKSLTLDDVPGY-GRVHFDGNSWYPSGRYKDRIFPANHVLPSQTPNPLRKYREE 199
DB 120 QYVLTLLIEDIPGHGDPVFNVCNSWYPAHYAHDVFFANKAYLPCHTEPELRKPREQ 179

QY 200 ELWNLRGDGTGERKEWDRIVDYVDNDIADPDVG-DH-RPILGGTTEVPYPRGRGTRPR 257
DB 180 ELKTLTCGFGKLNEDRVYDYAYNDJGLPDGDPDYARPVLGG-SQFPYPRGRGTRSRPH 238

QY 258 SRDRHNSRLSPIMSLDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLQSIQFVDTPN 317
DB 239 CKTDPKTESRLH-LNLNVYVPRDEQFGHVAFSDFLAYSLSKVAQVLLPEIKSLCDKTI 297

QY 318 EFDNPKVDNLFERGFPIPNNAFTLTEDLTP-PLFKALVRNDGKFLKEPTPEVVKDKN 376
DB 298 EFDTEQDVLDIYEGSIKLPSPGLTSKLRKLVPEYELLRELIRNDGERFLKFPVPDVKVSK 357

QY 377 IGWSTDESFAREMLAGNPLLRLEAPPTSKLDPNVYGNQNSTITEEHIKGLDGLTV 436
DB 358 TAWRTDESFAREMLAGNPNVIRRLQEPFPKSLDPSVIGDQTSIRATHIENSIDGLTI 417

QY 437 DEAMKQNLRYVDHDLAMPYLTRMNATSTKYATRTLLLLKDDGLTKPLVIELALPHQP 496
DB 418 DEAIQNMELFILDHHDHSLMPYISRINSTNTKYASRTLLFLQDDGTLKPLAIELSLPHQ 477

QY 497 GDQLCAISKLPFAENGQKSIWOLAKAYTVNDVGHQILSHLHHAVALPEPFIATNR 556
DB 478 GEQHGAVSKVTFPAQEGSVASVQWLAKAYAVNDVGHQVSHLVHLYTHAVLEPFIATNR 537

QY 557 QLSVLHPHKLIVPHYKDTFTINASARQVLINANGLIETTHYPSKYSMELSSILYKDWTF 616
DB 538 QLSILHPHKLKPHFRDTHMINALRHTLINAGVLEITVFPKGFALEMSVLYKSWVF 597

QY 617 PDQALPNMLKRGGLAVSDSAPHLRLINDYPAVDGLDIWSAIKTWQDYCCLYKDD 676
DB 598 TEQALPADLLKRGGAIPDSSSRHGLRVIEDYPAVDGIEIWDIAETWVTEYCNFYTSN 657

QY 677 NAVQNDPELQSWNELREKGHADKKHPPWPKMQTSELIESCTTIITWASALHAAVNF 736
DB 658 DMVEEDSELQSWKKEVRNEGHGDLKDRNWWPDMKTKEELIHSCTIILWASAFHAAVNF 717

QY 737 QYPYGYTLNRPTTSRPMPEBVGTAEYKELSPKAFLETICSELOALVSIIEILSK 796
DB 717 QYPYGYTLNRPTTSRPMPEBVGTAEYKELSPKAFLETICSELOALVSIIEILSK 796

Db 718 QYPAGYLPNRPVTSRRFMEQTPPEYBELKSDPELAFKXITTAQFOTLVGVSLIEVLSR 777
Qy 797 HASDEVYLGQASIDWTSKIALAEAFKFGKNLFVEVNRIMERKEVNLKXRGSPVNLPI 856
Db 778 HSTEYVLGQCEPENTLDAEPFLAERFRQKLEIENNIWERNKDKFRNRGPKVMPY 837
Qy 857 TLLVPSNE----GLTGRGIPNSISI 878
Db 838 TLLVPSNYSREGGLTKGIPNSISI 864

RESULT 13
US-10-424-599-220216
; Sequence 220216, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 220216
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(860)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40885C.1.pap
US-10-424-599-220216

Query Match 57.9%; Score 2706.5; DB 12; Length 860;
Best Local Similarity 59.9%; Pred. No. 4e-239;
Matches 513; Conservative 129; Mismatches 186; Indels 29; Gaps 7;

Qy 41 KIKKVLNRSNVLDFTEFIS-----NLLDNTELLGGVSVFQLISATHTSN 87
Db 14 KVKGTVMKRNKVLNDSINSVRGLGTGINIGTIDGLTSFLGRSVCLQLSATKADG 73
Qy 88 DSRGKVGNGKAYLERWLSIPPLFAGESVFOINFOWDENFGPGAFFIKNGHTSEFFLKS 147
Db 74 NNGVGVGKTYLEGIIISIPFLGAGQAFTHFEWDADMGIPGAFLLKYNQVLEFLVSL 133
Qy 148 TLDVPGVGRVHPCNSGNVPSGRYKXDRIPFANVHVLPSQTPNPLKRYEELNWLKRGD 207
Db 134 TLEDIPNQGMHFCVNSWVNSKYEKDRIFFASETYVPSETPGPLVTVREAEALQALRG 193
Qy 208 GTGRKEDWRIYDVNDIADPDVGDH--RPILGGTTEYVPRRGSTGRPRSRDHYE 265
Db 194 GTGRKEDWRIYDVNDIADPDVGDH--RPILGGTTEYVPRRGSTGRPRSRDHYE 253
Qy 266 SRLSPIMSLDTPVPCNENFGLKMSDFLGYTLKALSISIKPGLQSPDV--TPNEFDNF 323
Db 254 K-----PGEAYIPDENFGLKSSDFLYGLKSLTRSLPALKTVDINFTNEPDSFE 307
Qy 324 EVDNLFERGFPIPNAPKTLTETDLP-PLFKALVRNDGKELFPEVTVKDNKIGWSTD 382
Db 308 EVRALCEGKILPTD-----ILSKISPLPLVLEIFRTDGSVLPSPVDLLIKVSKAWMTD 363
Qy 383 BEFAREMLAGNPLILIRLEAFPPTSKLDPNVYQNSSTIEBHKHGLDGLTVDEAMQ 442
Db 364 BEFAREMIAGNVPVIRLQEPFPQSKLDPSVYGDQTSKMTIDHLEINLEGLTVDKAID 423
Qy 443 NRLYIVFDHDMPLVITMWN-ATSKTYATRTLLLLKDDGTLKPLVLEIALPHQGDQLG 501
Db 424 QRLFDLHDHDTFMPFLRIDESKSKAYATRTILFLKDDGTLKPLVLEIALPHQGDQLG 483

Qy 502 AISKLYFPAENGQVKSIVOLAKAYVTVNDVGHQLIISHWLHTHAVLEBPFVIATHRQLSVL 561
Db 484 AYSKVLFPANQGVSTIWLAKAHVIVNDSCVHQLISHWLHTHAVLEBPFVIATHRQLSVL 543
Qy 562 HPHKLLVPHYKDTWFINASARQVLINANGLIETTHYPSKSMELSSILYKDWTFPDQAL 621
Db 544 HPYKLLPFHYRDTWNINALARQSLINADGFIKTFGLGKYAVEISSSGYKNWFLDQAL 603
Qy 622 PNNLMKRGGLAVEDSSAPHGLRLINDYPAVDGLDINSAIKTWQDVCCLYYKDDNAYON 681
Db 604 PADLIKRGWATIEDSSCPNGLRLVIEDYPAVDGLEIDWAIKTWQVQVSVLYATNDALKK 663
Qy 682 DEELQSMNLEKEKHADKHEPMKQVOTSELTIESCTTIWITASALHAHVNGOYVYG 741
Db 664 DHELQAWKEVVERKGGDLKDKPMKQVOTLOELIQSCSTTIWITASALHAHVNGOYVYG 723
Qy 742 GYILNRPTTSRRFMEPEVGTAEYKELESNPEKAFRTICSELQALVSIISILSKHASDE 801
Db 724 GFILNRPTLSRWIPEEGTPEYDEMTKNPKQKAYLRTITPKQALVDLSVIELSRHASDE 783
Qy 802 VYLQORASIDWTSKIALAEAFKFGKNLFVEVNRIMERKEVNLKXRGSPVNLPIYLLVP 861
Db 784 VYLQORDNPNWTSNPKAEAFKFGKLABIETKISERNHDPNLRNRTGPAQLPYVLLP 843
Qy 862 SSNEGLTGRGIPNSISI 878
Db 844 TSSETGLTFRGIPNSISI 860

RESULT 14
US-10-424-599-239573
; Sequence 239573, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 239573
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_5835C.1.pap
US-10-424-599-239573

Query Match 57.8%; Score 2700.5; DB 12; Length 866;
Best Local Similarity 58.4%; Pred. No. 1.4e-238;
Matches 513; Conservative 127; Mismatches 195; Indels 43; Gaps 7;

Qy 23 VINAGNILDVRSSVGGNKIKGVILMRSNVLDFTEFH-----SNLL 64
Db 10 ILNRG-----GCHKIKGTVMKRNKVLNDFNSVADLTAKGNVGGGLIGTLNVLVSTL 59
Qy 65 DNFTTELLGGVSVFQLISATHTSNDSRGKVGKAYLERWLSIPPLFAGESVFOINFOWDE 124
Db 60 DNLTAFGRSVALQLISATKPLANGKVGKDKTFLGELIVSLPTLGAGESAFNIQFOWDE 119
Qy 125 NFGFTGAFPIKNGHTSEFFLKSILTDDVPGYGRVHFDCNSWYPSGRYKXDRIPFANHY 184
Db 120 SMGIFGAFYIKYNQVVEFLKSLTLEDVFNQGTIRFCVNSWYNTKLYKSVRIFPANTY 179
Qy 185 LPSQTPNPLKRYEELNWLKRGDGTGRKEDWRIYDVNDIADPDVGDH--RPILGGT 242
Db 180 VPSQTPNPLKRYEELNWLKRGDGTGRKEDWRIYDVNDIADPDVGDH--RPILGGT 239

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OM protein - protein search, using sw model

Run on: July 16, 2004, 11:51:28 / Search time 40.0332 Seconds
(without alignments)
2109.655 Million cell updates/sec

Title: US-09-937-908-1
Perfect score: 4675
Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVPSNBLRGRGIPNSISI 878

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4675	100.0	878	2 S74207	lipoxigenase (EC 1
2	3657.5	78.2	877	2 T10085	lipoxigenase (EC 1
3	2948.5	63.1	862	2 T07775	lipoxigenase (EC 1
4	2932	62.7	861	2 S44940	lipoxigenase (EC 1
5	2911	62.3	862	2 S57964	lipoxigenase (EC 1
6	2847	60.9	859	1 JQ2267	lipoxigenase (EC 1
7	2813.5	60.2	859	2 T06352	lipoxigenase (EC 1
8	2812.5	60.2	859	2 T06339	lipoxigenase (EC 1
9	2776	59.4	857	2 S01864	lipoxigenase (EC 1
10	2705.5	57.9	864	1 S07075	lipoxigenase (EC 1
11	2705	57.9	876	2 T07101	lipoxigenase (EC 1
12	2696.5	57.7	861	1 S01142	lipoxigenase (EC 1
13	2690	57.5	865	1 DASV11	lipoxigenase (EC 1
14	2663	57.0	865	2 T11852	lipoxigenase (EC 1
15	2649	56.7	859	2 T06429	lipoxigenase (EC 1
16	2644.5	56.6	864	2 S13381	lipoxigenase (EC 1
17	2640.5	56.5	858	2 T12142	lipoxigenase (EC 1
18	2634.5	56.4	856	2 T06596	lipoxigenase (EC 1
19	2632.5	56.3	868	2 T06837	lipoxigenase (EC 1
20	2596	55.5	862	2 S22153	lipoxigenase (EC 1
21	2591	55.4	853	2 T07662	lipoxigenase (EC 1
22	2582.5	55.2	839	1 DASV02	lipoxigenase (EC 1
23	2577	55.1	853	2 T07036	lipoxigenase (EC 1
24	2571	55.0	839	2 T06354	lipoxigenase (EC 1
25	2567	54.9	866	2 T06454	probable lipoxigen
26	2494.5	53.4	868	2 S56655	lipoxigenase (EC 1
27	2438	52.1	862	2 T05941	lipoxigenase (EC 1
28	2424	51.9	864	2 T05945	lipoxigenase (EC 1
29	2415	51.7	741	2 S18906	lipoxigenase (EC 1

30	2390.5	51.1	865	1 S23454	lipoxigenase (EC 1
31	2378	50.9	876	2 T05943	probable lipoxigen
32	1929.5	41.3	599	2 S18612	lipoxigenase (EC 1
33	1869	40.0	914	2 T07065	probable lipoxigen
34	1843	39.4	908	2 T07409	lipoxigenase (EC 1
35	1822.5	39.0	926	2 E96749	probable lipoxigen
36	1759.5	37.6	899	2 T07062	probable lipoxigen
37	1740	37.2	896	2 JQ2391	lipoxigenase (EC 1
38	1740	37.2	899	2 T11578	probable lipoxigen
39	1737.5	37.2	896	2 T07408	lipoxigenase (EC 1
40	1674	35.8	917	2 B96699	probable lipoxigen
41	1652	35.3	923	2 A53054	lipoxigenase (EC 1
42	1629	34.8	870	2 T47454	lipoxigenase AtLOX
43	1568.5	33.6	517	2 T06274	probable lipoxigen
44	1562	33.4	623	2 T07664	lipoxigenase (EC 1
45	1532.5	32.8	936	2 T06190	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1

S74207
lipoxigenase (EC 1.13.11.12) - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: S74207; S74137
R;Hoehne, M.; Nellen, A.; Schwennesen, K.; Kindl, H.
Eur. J. Biochem. 241, 6-11, 1996
A;Title: Lipid body lipoxigenase characterized by protein fragmentation, cDNA sequence
A;Reference number: S74137; MUID:97054584; PMID:889881
A;Accession: S74207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-878 <HOE>
A;Cross-references: EMBL:X92890; NID:G1296511; PIDN:CA63483.1
A;Experimental source: tissue cotyledones; clone PCSLBLOX221
A;Accession: S74137
A;Molecule type: protein
A;Residues: 196,'X',198-204;218,'FX',221-223,'XX',226-228;305-309,'XX',312-316;441-460;
C;Superfamily: lipoxigenase
C;Keywords: oxidoreductase

Query Match	100.0%;	Score	4675;	DB 2;	Length	878;	
Best Local Similarity	100.0%;	Pred. No.	1e-310;				
Matches	878;	Conservative	0;	Mismatches	0;	Gaps	0;
QY	1	MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGKNIKGKVIILMRSNVLDTEFH	60				
Ddb	1	MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGKNIKGKVIILMRSNVLDTEFH	60				
QY	61	SNLLDNFTELLGGVVSFQLISATHTSNDSRGKVGKNAYLERWLTSIPPLFAGESVFQINF	120				
Ddb	61	SNLLDNFTELLGGVVSFQLISATHTSNDSRGKVGKNAYLERWLTSIPPLFAGESVFQINF	120				
QY	121	QNDENFGPGAFFIKNGHTSEFFLKSLTLDVPGYGRVHFDNCNSWYVPSGRYKKDRIFFA	180				
Ddb	121	QNDENFGPGAFFIKNGHTSEFFLKSLTLDVPGYGRVHFDNCNSWYVPSGRYKKDRIFFA	180				
QY	181	NHVILPSQTPNPLRKRYEEELWNLRGDTGERKEWDRIYDYDVYNDIADPVDGDRHPILG	240				
Ddb	181	NHVILPSQTPNPLRKRYEEELWNLRGDTGERKEWDRIYDYDVYNDIADPVDGDRHPILG	240				
QY	241	GTTTEYPYPRGRGTRPRSRDRDHNYESRLSPIMSLDIYVPKDNFNGHLKMSDFLGTYLKAL	300				
Ddb	241	GTTTEYPYPRGRGTRPRSRDRDHNYESRLSPIMSLDIYVPKDNFNGHLKMSDFLGTYLKAL	300				
QY	301	SISIKPGQLSIFDVTPEFNDFKEVDNLFERGFPIPFNAFKTLTDLTPPLFKALVRNDG	360				
Ddb	301	SISIKPGQLSIFDVTPEFNDFKEVDNLFERGFPIPFNAFKTLTDLTPPLFKALVRNDG	360				
QY	361	EKFLKFTPTPEVVKDKNIKGSWDEEFAREMLAGNPILLIRLEAFPTPSKLDPNVYGNQNS	420				

Db 361 EKLFKPTPEVVYKONKIGWSTDEFAREMLAGNPLLIIRLEAPPTSKLDPNVYGNQNS 420
 QY 421 TITEBHIKHGLDGLTVDEAMKONLXIYVDFHDLMPYLTRMNATSTKYATRTLLIKDD 480
 Db 421 TITEBHIKHGLDGLTVDEAMKONLXIYVDFHDLMPYLTRMNATSTKYATRTLLIKDD 480
 QY 481 GTLPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWQLAKAYVTVNDVGHQLISHW 540
 Db 481 GTLPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWQLAKAYVTVNDVGHQLISHW 540
 QY 541 LHTHAVLEPFIATHRQSLVLPHTHKLAVPHYKDTMFINASAROVLINANGLIETHYPS 600
 Db 541 LHTHAVLEPFIATHRQSLVLPHTHKLAVPHYKDTMFINASAROVLINANGLIETHYPS 600
 QY 601 KYSMELSSILYKDWTFPPQALPNNLMKRGSLAVEDSSAPHGLRLLLINDYPPAVDGLDIWSA 660
 Db 601 KYSMELSSILYKDWTFPPQALPNNLMKRGSLAVEDSSAPHGLRLLLINDYPPAVDGLDIWSA 660
 QY 661 IKTWQDYCCLYYKDDNAVQNDPELOSWWNELEKRGHADKKHBPWPKMOTLSLIESCT 720
 Db 661 IKTWQDYCCLYYKDDNAVQNDPELOSWWNELEKRGHADKKHBPWPKMOTLSLIESCT 720
 QY 721 TIITIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAPLRTICS 780
 Db 721 TIITIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAPLRTICS 780
 QY 781 ELQALVSIIEILSKHASDEVYLGORASIDWTSKIALEAFKFGKVLFEVENRIMERN 840
 Db 781 ELQALVSIIEILSKHASDEVYLGORASIDWTSKIALEAFKFGKVLFEVENRIMERN 840
 QY 841 KEVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 878
 Db 841 KEVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 878
 RESULT 2
 T10085
 lipoxigenase (EC 1.13.11.12) - cucumber
 C:Species: Cucumis sativus (cucumber)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T10085
 R:Matsui, K.; Mishioke, M.; Kajiwara, T.; Hase, T.
 submitted to the EMBL Data Library, September 1995
 A:Reference number: Z16939
 A:Accession: T10085
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-877 <MAT>
 A:Cross-references: EMBL:U36339; NID:g1017771; PID:g1017772
 A:Experimental source: cv. Suoyo; tissue type root
 C:Function:
 A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis per
 C:Superfamily: lipoxigenase
 C:Keywords: fatty acid oxidation; oxidoreductase
 Query Match 78.2%; Score 3657.5; DB 2; Length 877;
 Best Local Similarity 76.2%; Pred. No. 2.7e-241;
 Matches 671; Conservative 105; Mismatches 99; Indels 5; Gaps 4;
 QY 1 MFGIGKNIIEGALNTTGLAGSVINAGGNILDRVSSLGKNIKGVILMRSNVLDTFEPH 60
 Db 1 MFSIGNIIEGALNTTGLAGSVINAGGNIAQDSNIGGQIKGVILMRSNVLDTFEPH 60
 QY 61 SNLLDNFTLEGGVSVFOLISATHTSN-DSRGKVNKAYLERWLTSTIPPLPAGESVFOIN 119
 Db 61 SLLDNFTLEGGVSVLQISATQTSALDSRGVKAKFLERWLTSTIPPLPAGESVFOQS 120
 QY 120 FQWDSNFGPGGAFFIKNGHTSEFFLKSLTLDVPGYGRVHFDCNSWYPSGRYKDKRIFF 179
 Db 121 FTWEGFPGPGAFFIKNGHTSEFFLKSLTLDVPGYGRVHFDCNSWYPSGRYKDKRIFF 180
 QY 180 ANHVLPSTQPNPLRYREELWNLRGDTGERKEWDRIYDYVNDIADPDVGDHPIL 239

Db 181 ANNTVLPSTQPNPLRYREELWLRGDTGERKEWDRIYDYVNDIADPDVGDHPIL 238
 QY 240 GGTTEYPYPRGRTRGRPRSRDHNYESRLSPIMSLDIYVVKDENFGHLKMSDFLGYLTKA 299
 Db 239 GG-SQFPYPRGRTRGRPREWKSDNYESRLPVVSGLINIYVPRDENFGHLKMSDFLGALKS 297
 QY 300 LSISIKPGQLOSTFDVTPNEFDNFKEVDNLFERGPPIENAKPTLTEDLTPLFKALVRND 359
 Db 298 LVATVQPALNIVDFTPGFDFKQVHNLVYEGGVPVLDVFNRLTKDTTPMFFBELRTD 357
 QY 360 G-EKELKPTPEVVYKONKIGWSTDEFAREMLAGNPLLIIRLEAPPTSKLDPNVYGNQ 418
 Db 358 NDQRELFKSPQVVKEDKFAQOTDEFAREMLAGNPLLIIRLEKFPKSKLDPMYGDQ 417
 QY 419 NSTIITEHIIKHGLDGLTVDEAMKONLXIYVDFHDLMPYLTRMNATSTKYATRTLLIK 478
 Db 418 HSKITEEDIKSGLEGLTVAEALNQRLYLIDHDLMPYLTRKINSTKTKTATRTLLIK 477
 QY 479 DDGTLKPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWQLAKAYVTVNDVGHQLIS 538
 Db 478 NDGTLKPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWQLAKAYVTVNDVGHQLIS 537
 QY 539 HMLHTHAVLEPFIATHRQSLVLPHTHKLAVPHYKDTMFINASAROVLINANGLIETHY 598
 Db 538 HMLHTHAVLEPFIATHRQSLVLPHTHKLAVPHYKDTMFINASAROVLINANGLIETHY 597
 QY 599 PSKYSMELSSILYKDWTFPPQALPNNLMKRGSLAVEDSSAPHGLRLLLINDYPPAVDGLDIW 658
 Db 598 QSKYAMELSSYIYKDWTFPPQALPNNLMKRGSLAVEDSSAPHGLRLLLINDYPPAVDGLDIW 657
 QY 659 SAIKTWQDYCCLYYKDDNAVQNDPELOSWWNELEKRGHADKKHBPWPKMOTLSLIES 718
 Db 658 STIKTWVNYCSLYYKDDSAIQNDVLEQSWWKEVREKGVKDKONETWPKLQNFELVET 717
 QY 719 CTIIIIWIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAFRTI 778
 Db 718 CTIIIIWIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAFRTI 777
 QY 779 CSELOALVSIIEILSKHASDEVYLGORASIDWTSKIALEAFKFGKVLFEVENRIME 838
 Db 778 NSMLQTLGLVSLIIEILSKHASDEVYLGORASIDWTSKIALEAFKFGKVLFEVENRIME 837
 QY 839 RNKEVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 878
 Db 838 RNKDVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 877
 RESULT 3
 T07775
 lipoxigenase (EC 1.13.11.12) LX-3 - potato
 C:Species: Solanum tuberosum (potato)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
 C:Accession: T07775
 R:Kolomietz, M.V.; Hannapel, D.J.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z16124
 A:Accession: T07775
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-862 <KOL>
 A:Cross-references: EMBL:U60202; NID:g1407704; PIDN:AA867865.1; PID:g1407705
 A:Experimental source: cv. Barolina
 C:Genetics:
 A:Gene: LX-3
 C:Function:
 A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis per
 C:Superfamily: lipoxigenase
 C:Keywords: fatty acid oxidation; oxidoreductase
 Query Match 63.1%; Score 2948.5; DB 2; Length 862;
 Best Local Similarity 63.2%; Pred. No. 6.3e-193;
 Matches 534; Conservative 138; Mismatches 166; Indels 5; Gaps 3;

QY 39 GNKIKGVILMRNVLDTEPHSNLNDNFTELLGGGVSPOLISATH--SNDSEKGVGNK 96
Db 18 GKVKYGVILMKKNVLDNFNDNASLSDGVLEFLGKRVSLQSLISVHADPGNSLQGRSNP 77
QY 97 AYLERWLTISIPPLFAGSVFQINQWDFENFGFPAGFIKNGHSTSEFFELKSLITLDDVPGYG 156
Db 78 AYLEKWLITGSLVAGESAFDVTFDWDEDIGVPCAFIINPHFNEFYKLSLITLEDVPHG 137
QY 157 RVHFDCHSVWYPSGRYKDKRIFFANHYLPSQTNPLRKRYREBELNWLNRGCGTGERKEWD 216
Db 138 NVHFVCSWVYPAKKYSERIFFANQAYLPOETPEPLRNYREBELNWLNRGNGKLEBWD 197
QY 217 RIYDYVDVNDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPSRDHNYESLSPTMSL 274
Db 198 RYDYALYNDIGDEKQKQYARTILGSAEYYPYPRGRGTGRKPKADPKSESRIPLMSL 257
QY 275 DIYPKDNFGLKMSDFGLYTLKALSISIKPGLQSIQIDVTPNEFDFKXVDNLFERGFP 334
Db 258 DIYPVPRDFRFGHILKSLDFLTALKSIVQFLIPEFQALFDSPTDFDFEDFEDVLKLYEGGK 317
QY 335 IFFNAF--KTLTDEDTPPLFKALVNDGKFLKPTPTPVVKNKIGWSTDEEFAREMLAGP 393
Db 318 LPQGFFLKALDTSIPLEIKELIITDGEKFKFTPTPOIQEDKSGWSTDEEFAREMLAGV 377
QY 394 NPLLRLEAPPTSKLDPNVYGNQNSTITEEHKHLGDLGLTVDKAMQNRLYIVDPHDA 453
Db 378 NPVIISRLQEPFKSOLDSSEVYGNQNSTITKEHIENTLDGLTIDDAIKTNRLYILNHDI 437
QY 454 LMPYLTRMNAATSKTYATRLILLKDDGTLPKPLVIELALPHPOQDGLGALSILYFPAENG 513
Db 438 LMPYVRRINTNTKLYASRTLFLQDDGTWKPVAIELSLPHDPGDGLGAVSKVYTPADQG 497
QY 514 VQKSIWOLAKAYVTVNDVGVHQLISHWLHVALEPPVVIATHRQLSVLHPIHKLIVPHYK 573
Db 498 VEGSIWOLAKAYVAVNDVGVHQLISHWLHVALEPPVVIATHRQLSVLHPIHKLHPHR 557
QY 574 DTMFINASARQVLINAGLLETHYPSKYSMELSSILYKDWTPPDQALPNMLMKRGLAVE 633
Db 558 DTMNALARQILINAGLVLEMTVPKAYAMEMSAVYKSVWPEQALPADLIRKGVAVE 617
QY 634 DSSAPHLRLINYPYPAVDGLDLSWAIKTVWQDYCCLYKDDNAVQNDPELOSNNELR 693
Db 618 DSSSPHGVRLLIQYYPYAVDGLSLWSAIKSNVTEYCNFYKSDLVKDNELQANWKELR 677
QY 694 EKHGADKXHEPWPWKMTLSLIESCTTIIWIASALHAANVFGQYPGGYILNRPITSRR 753
Db 678 BEGHGDKDEPWPWKMTQRLKDSCTIIWIASALHAANVFGQYYPAGYLPNRPITLSRR 737
QY 754 FMPVGTAEYKESNEPEKFLRTICSELQALVSIISIIELSKHASDEVYLGORASIDWT 813
Db 738 FMPSPGTPEYBELKTNPDKAYLKTITPOLQTLGSLIIEILSRHASDEIYLGORDSEWT 797
QY 814 SDKIALFAFEKGNLFEVENRIMERNEKVNLRSGPVNLPTYTLVPSSNEGILTKRGIP 873
Db 798 KDQSPIAAFERFGKLSIEIDQIIQMGDKKKNRSGPVNVVPTLLPFTSEQGLTKGIP 857
QY 874 NSISI 878
Db 858 NSVSI 862

RESULT 4

S44940
lipoxigenase (EC 1.13.11.12) - potato
C:Species: Solanum tuberosum (potato)
C:Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C:Accession: S44940
R:Casey, R.
submitted to the EMBL Data Library, May 1994
A:Reference number: S44940
A:Accession: S44940
A:Molecule type: mRNA
A:Residues: 1-861 <CAS>

A;Cross-references: EMBL:X79107; NID:G486618; PIDN:CAA55724.1; PID:G486619
C;Superfamily: lipoxigenase
C;Keywords: oxidoreductase

Query Match 62.7%; Score 2932; DB 2; Length 861;
Best Local Similarity 63.8%; Pred. No. 8.4e-192;
Matches 543; Conservative 124; Mismatches 174; Indels 10; Gaps 5;

QY 38 GGN----KIKGVILMRNVLDTEPHSNLNDNFTELLGGGVSPOLISATH--TSNDRG 91
Db 11 GGHDSKKVKGTVVMNKNVLDFTDLAGSLTGKIFDVLGQKVSFQLISSVQDPTNGLQG 70
QY 92 KVGNKAYLERWLTISIPPLFAG--ESVFQINQWDFENFGFPAGFIKNGHSTSEFFELKSLITLD 150
Db 71 KSNPAYLENSLFTITPLTAGSETAFGVTFDWNBEFVGPGAFIKNMGINFEFLKSLITLD 130
QY 151 DYPVGRVHFDCHSVWYPSGRYKDKRIFFANHYLPSQTNPLRKRYREBELNWLNRGCGTG 210
Db 131 DVNHEGKHFVCSWVYPSLNYKSDRIFFANQYLPSETPELLRKYRENEILLRAGDGTG 190
QY 211 ERKEWDRIYDYVDVNDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPSRDHNYESRL 268
Db 191 KKEAWDRIYDYVDVNDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPSRDHNYESRL 250
QY 269 SPIMSLDIYVPKDNFGLKMSDFGLYTLKALSISIKPGLQSIQIDVTPNEFDFKXVDNL 328
Db 251 PLISLSDIYVPRDERFGLKMSDFLTALKSIVQFLIPELHALPDGTNEFDFEDVLRL 310
QY 329 FERGPPIPN--AFKILTDETLPLPKALVNDGKFLKPTPTPVVKNKIGWSTDEEFAR 387
Db 311 YEGGKLPQGPLFKALTAAPLEMIRELLRTDGEILRFPTPLVIKDKSTAWRTDEEFAR 370
QY 388 EMLAGNPLLIIRLEAPPTSKLDPNVYGNQNSTITEEHKHLGDLGLTVDKAMQNRLYI 447
Db 371 EMLAGNVPIISRLQEPFKSOLDSSEVYGNQNSTITAEHIEDKLDGLIVDEAMNNKLF 430
QY 448 VFHDMPLTRMNAATSKTYATRLILLKDDGTLPKPLVIELALPHPOQDGLGALSILY 507
Db 431 LNHHDVILPYLRINTITKAYASRTLFLQDNGSLKPLAIELSPHPDQGFVTSKVY 490
QY 508 FPAENGVOKSIVQALAKAYVTVNDVGVHQLISHWLHVALEPPVVIATHRQLSVLHPIHKL 567
Db 491 TFSQGVRESSIVQALAKAYVAVNDVGVHQLISHWLHVALEPPVVIATHRQLSVLHPIHKL 550
QY 568 LVPHYKDTMFINASARQVLINAGLLETHYPSKYSMELSSILYKDWTPPDQALPNMLMK 627
Db 551 LYPHFRDTMNINASARQLLVNAGVLESTVFQSKFAMEMSAVYKDWVFPDQALPADLVK 610
QY 628 RGLAYEDSSAPGLBLLINDYPPAVDGLDLSWAIKTVWQDYCCLYKDDNAVQNDPELOS 687
Db 611 RGVAVEDSSPHGVRLLIEDYYPYAVDGLSLWSAIKSNVTEYCSFYGSDEEILKDNELQA 670
QY 688 WNNELREKGHADKXHEPWPWKMTLSLIESCTTIIWIASALHAANVFGQYPGGYILNR 747
Db 671 WKELREVGHGDKKNPWPWPEMETPQELIDSCITIIWIASALHAANVFGQYYPAGYLPNR 730
QY 748 PTSSRRFMPVGTAEYKESNEPEKFLRTICSELQALVSIISIIELSKHASDEVYLGOR 807
Db 731 PTSSRRFMPVGTAEYKESNEPEKFLRTICSELQALVSIISIIELSKHASDEVYLGOR 790
QY 808 ASIDWTSKIALFAFEKGNLFEVENRIMERNEKVNLRSGPVNLPTYTLVPSSNEGIL 867
Db 791 ESPFWTKKEPLAADFRCFKLTDIEKQIIQRNGDNILTRNSGPNVAPYTLFPFSEGL 850
QY 868 TCRGIPNSISI 878
Db 851 TCRGIPNSVSI 861

RESULT 5

S57964
lipoxigenase (EC 1.13.11.12) - common tobacco
C:Species: Nicotiana tabacum (common tobacco)

C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jun-1999
C/Accession: S57964
R:Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.
submitted to the EMBL Data Library, January 1995
A/Description: Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA.
A/Reference number: S57964
A/Accession: S57964
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-862 <VER>
A/Cross-references: EMBL:X84040; NID:G899343; PIDN:CAA58859.1; PID:G899344
C/Superfamily: lipoxigenase
C/Keywords: oxidoreductase

Query Match 62.3%; Score 2911; DB 2; Length 862;
Best Local Similarity 62.3%; Pred. No. 2.3e-190;
Matches 534; Conservative 140; Mismatches 175; Indels 8; Gaps 6;
QY 30 ILDRVSSL-GNKIKGKVKYKILMRNVLDTEPHSNLLDNFTFELGGVSLFOLIGATHT--S 86
DB 6 IVDALTGDDGKKYKGTIVLMKNVLDFTDINASVLDGVLEFLGRRVSLSELISVNAADPA 65
QY 87 NDSRGKGNKAYLERWLTISPLPAGESVFOINFOW-DENPGFPGAFFIKNGHTSEFFLK 145
DB 66 NGLOGKRAKAYLENWLTNSTPIAAGESAFRTVDWDEBFGVPGAFIINKLHFSFFLK 125
QY 146 SLTLDVDPVGRVDFCNVSPGRYKORIPFANHVLPSQTPNPLRYKREELWNL 205
DB 126 SLTLEDVNHGKVFVCMVSWYPANKYKSDRIFFANQAYLPSETPDLRKIRENELVTLR 185
QY 206 GDGTGERKEDRIYDYNDIADPDVGD--HRLIGGTTTEYPYPRGRGTRGRSRADHN 263
DB 186 GDGTGKLEWDRVYDAYNDLGDPDGQDLSRPVGLSGSEYYPYPRGRGTRGRPTKDPN 245
QY 264 YESRLSPMSLDIYVPKDNFCHLKMDFLGYTLKALSISIKPGLQSFIDVTNPFNF 323
DB 246 SESRIPLMSLDIYVPRDERFGHLKSDFLTFAUKSIVQLLPBFKALFDSITNEFDSFE 305
QY 324 EVDNLFRGFPIPFN-APKTTEDLTPLFKALVRNDGKFLKPTPEVVKDNKIGWSTD 382
DB 306 DVLKLYEGGKLPQGPLLKAITDSIPLEILKELARSDEGLFKYPTPVQLQEDKTAWRTD 365
QY 383 BEFAREMLAGNPILRLREAFPTSKLDPNVYGNQNSTITEEHIKGLDGLTVDEAMQ 442
DB 366 BEFGREMLAGNPVILISLQEPFKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEA 425
QY 443 NRLIYVDFHDMALPVLTMN-ATGKTATYATRLLLKDDGLTKPLVTELALPHPQGDQLG 501
DB 426 NRLFILNHHDLMPYLRLINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHPDGDOFG 485
QY 502 AISKLYFPAENGVOKSIWQAKAYTVNDVGVYHOLISHWLTHAVLEPPIATHRQLSVL 561
DB 486 AVSKYVTPADQGVSGSIWQAKAYAVNDVGVHOLISHWLTHAAIEPPIATHRQLSAL 545
QY 562 HPIKLIAPHYKDMFNINASARQVLINANGIETTHYPSKYSMELSSILYKDMTFPQDAL 621
DB 546 HPIYKLLHPHRETWNINARQVLINGGGGLEUTVPKYSMBMSAVVYKDWVFPPEQAL 605
QY 622 FNNLMKRGVAVEDSSAPHGLRLINDYPAFVGDGLDINSAIKTWQDYCCLYKDDNAVQN 681
DB 606 PTDILKRGVAVEDSSPLGIRLLIQQDYPAVDGLKWSAISKWSWTEYCNYYKSDDAVQK 665
QY 682 DFELOSNNELREKHADKKEHPWPKMOTLSIELSCITTIINTASALHAANVFGQPYG 741
DB 666 DTELQAMWKEURESGHGDKDEPWWPKMOTVQELISDCTITTIINTASALHAANVFGQPYA 725
QY 742 GYLNRPTTSRRFPEVGTAEYKELSNPEKAFRLTICSELQALVSIISIELLSKIASDE 801
DB 726 GYLNRPTLSNFMFPERGSPYEELKTPDKVFLKTTIPQLQTLGLISIELLSRHSST 785
QY 802 VYLQASIDNTSKIALAEFEKGNLFVENRIMERNKEVNLKNSGPNVLPYLLVP 861
DB 786 LYLQGRESPEWTKQEPISAFAREGKKLSIDEDIQIMQNVDEKWKNSRGPVKPYTLLFP 845

QY 862 SSNEGLTGKIPNSISIS 878
DB 846 TSEGGLTGKIPNSVSI 862

RESULT 6

QJ02267
lipoxigenase (EC 1.13.11.12) Lox1 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: JQ2267
R/Melan, M.A.; Dong, X.; Endara, M.E.; Davis, K.R.; Ausubel, F.M.; Peterman, T.K.
Plant Physiol. 101, 441-450, 1993
A/Title: An Arabidopsis thaliana lipoxigenase gene can be induced by pathogens, abscisic
A/Reference number: JQ2267; MUID:94105302; PMID:7506426
A/Accession: JQ2267
A/Molecule type: mRNA
A/Residues: 1-859 <MEL>
A/Cross-references: GB:L04637; NID:G289202; PIDN:AAA32827.1; PID:G289203
C/Comment: This enzyme catalyzes the hydroperoxidation of polyunsaturated fatty acids co
C/Superfamily: lipoxigenase
C/Keywords: fatty acid oxidation; oxidoreductase

Query Match 60.9%; Score 2847; DB 1; Length 859;
Best Local Similarity 61.0%; Pred. No. 5.3e-186;
Matches 525; Conservative 142; Mismatches 181; Indels 12; Gaps 7;
QY 28 GNILDRVSSLGN-----KIRGKILMRNVLDTEPHSNLLDNFTFELGGVSLFOLISA 82
DB 3 GELRDLLTG-GGNETTTTKVGTIVLMKNVLDNFNFASFLDLRHLHEFLGNKILRLVSS 61
QY 83 --THTSNDSRGKGNKAYLERWLTISPLPAGESVFOINFOWDENFPPGPAFFIKNGHTS 140
DB 62 DVTDSENGSKGLKAAHLEDNITITSLTAGESAFKVTYDFTDFGVPGLFIENSHFS 121
QY 141 EFPLKSLTLDVPGVGRVHFCNSVYPSGRYKDKRIPFANHVLPSQTPNPLRYKREEE 200
DB 122 EFLLKSLTLEDVPGHGRVHYTCSNWIYPAKHYTTDRVFFSNKTYLPHETATLLKYRREE 181
QY 201 LWNLRGDTGGRKEDRIYDYNDIADPDVGRHPLTGGTTEYPYPRGRGTRGRSRR 260
DB 182 LVSLRGTEGELKEDRVIDYAYNDLGVPP-KNRPVVLGGTQYYPYPRGRGTRGKTKE 240
QY 261 DHNYSRLSPIMSLDIYVPKDNFCHLKMDFLGYTLKALSISIKPGLQSFIDVTNPFNEFD 320
DB 241 DPQTESRLPITSSLDIYVPRDERFGHLKMDFLALYAKAIAQFIQPALEAVFDDTPKEFD 300
QY 321 NFEKVDNLPFSGFPIPFNA-FKLTLEDLTPLFKALVRNDGKELKPTPEVVKDNKIGW 379
DB 301 SPEDVLKIYEGIDILFNQALIDSIVKNIPLEMLKEIFRDCGKFLKFPVPVVKEDKTAW 360
QY 380 SPDEFAREMLAGNPILRLREAFPTSKLDPNVYGNQNSTITEEHIKGLDGLTVDEA 439
DB 361 RTDEFAREMLAGNPVILQLKBPFPKSKLDSYGNQNSTITKSHIEHNLGLTVEEA 420
QY 440 MKQNLRIYVDFHDMALPVLTMNATSTKYATRLILLKDDGTLKPLVIELALPHPOGDO 499
DB 421 LEKERLFLDHHDTLMPYLGRVNTTITKYASRTLLFLKDDGTLKPLVIELSLPHHPGDK 480
QY 500 LGAISKLYFPAENGVOKSIWQAKAYTVNDVGVYHOLISHWLTHAVLEPPIATHRQLS 559
DB 481 FGAVSEVTPGE-GYVDSLWQLAKAFVGVNDVSGNQLISHMWMQTHASTEPVIATNQLS 539
QY 560 VLHPILKLLVPHYKDMFNINASARQVLINANGIETTHYPSKYSMELSSILYKDYD-WTFPD 618
DB 540 VLHPYFKLLEPHFRTWNINARQVLINGGGGLEUTVPKYSKYAMEMSSFIYKHNWTFPD 599
QY 619 QALPNLMKRGVAVEDSSAPHGLRLINDYPAFVGDGLDINSAIKTWQDYCCLYKDDNA 678
DB 600 QALPAELKRGVAVEDPEAPHGLRLIKDYPAVDGLEVWVAIESWVRDYLFLYKLEED 659
QY 679 VONDELOSNNELREKHADKKEHPWPKMOTLSIELSCITTIINTASALHAANVFGQY 738

Db 660 IOTTELOAWKEVREGEHGDKKPEWPKMOTREELVESCTIIWASALHAAVNGQY 719
QY 739 PYGGLNRPRTTSRRFPEVGTATYKELESNPEKAFRTICSELOALVSIISIIILSKHA 798
Db 720 PVAGYLPNRPISRYQPKENTPEFELEKNPKDFVLKTTIAQQLTGLISLIIILSTHS 779
QY 799 SDEVYLGORASIDWTSKIALEAFKFGKKNLFEVENRIMERNEKVNKNSGPNVLYTL 858
Db 780 SDEVYLGORDSKWAEEKALEAFKFGKKEIEKNIDERNDDTLKNTGLVMEYTL 839
QY 859 LVPSNEGLTGRGIPNSISI 878
Db 840 LFPSEGGVTGRGIPNSVSI 859

RESULT 7
T06352
lipoxigenase (EC 1.13.11.12) - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
A:Accession: T06352
R:Kausch, K.D.; Handa, A.K.
Plant Physiol. 107, 669-670, 1995
A:Title: Molecular cloning and nucleotide sequence of a lipoxigenase cDNA from ripening
A:Reference number: Z15617; MUID:95241637; PMID:7724686
A:Accession: T06352
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-859 <KAU>
A:Cross-references: EMBL:U13681; NID:9534845; PIDN:AAA74393.1; PID:9534846
A:Experimental source: strain Rutgers; tissue-type fruit pericarp
C:Genetics:
A:Gene: LOX
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 60.2%; Score 2813.5; DB 2; Length 859;
Best Local Similarity 60.9%; Pred. No. 1e-183;
Matches 523; Conservative 140; Mismatches 185; Indels 11; Gaps 7;

QY 28 GNILDRVSSLGNN--KIKGVILMRNVLDFTFEHNLNDNFTLGGVSGVQLISATH 84
Db 4 GGIVDAI--LGKDRPKVKGKVLMMKNVLDFTINIGASVVDGSLDLGGVSGVQLISGV 61
QY 85 TSNDRGKGVGNKAYLERWLTISIPPLFAGESVFQINFQWD--ENFGPFGAFFIKNGHTSEFF 143
Db 62 NYDGLGKLSNPAYLESWLTIDITPITAGESTFSVTFDWRDEFQVPGAFIKNLHNEFF 121
QY 144 LKSLTLDDVPGYGRVHFDGNSWVPSGRYKDKRIFFANHVLPSTQNPPLRKYREELWN 203
Db 122 LKSLTLEDVPGYGRVHFDGNSWVPSGRYKDKRIFFANHVLPSTQNPPLRKYREELVA 181
QY 204 LRGGDTGERKEWDRIYDVYNDIADPDVGDH--RPILGGTTEYPYPRGRGRPRSRD 261
Db 182 LRGGDTGKLEWDVYACVNDLGECDKGEYARPIILGSGSEYFYPGRGRGREPTKAD 241
QY 262 HNYESRSPIMSLDIYVPKDNFGLKQSDPLGLVTLKALISIKPGLQSFIVPTNPFEDN 321
Db 242 PNCESRNPPLMSLDIYVPRDRFRGHVKKSDPLTSLKSLQTLPLFAFKALCDNTPEFNS 301
QY 322 FKEVDNLPGRGFPFENAF--KTLTETDLPPLFKALVNDGEGKFLKFTPEVVKDNKIGWS 380
Db 302 FADVLNLYEGGIKLPFGFWLKAIDNISSEILKQILQTDGGLGLKYTPQVIOGDKTAWR 361
QY 381 TDEFAREMLAGPNLLIRLEAPPTSKLDPNYGNQNSITTEHFKHGLDGLTVDEAM 440
Db 362 TDEFBGRMLAGSNPLVLSRLQSEFPKSKLDPTIYGNQNSITTEHVQDKLGLTVNEAI 421
QY 441 KQNELYIVDFDALMPYLTRNN--ATSTKTVATRLALLKODGTGLKPLVIELALPHPOGQ 499
Db 422 KSNRLFILNHDIIVNPLLRKINNSANTKAYASRTLLFLQDDRTLUKPLAIELSUPHPDQ 481

QY 500 LGAISLKYPPAENGQVQKSIWQIAKAYTVTVNDVGYHQLISHWLTHTAVLEPFIATHROLS 559
Db 482 FGTQSVKYVTPADOGVEGSIWQFAKAYAVANDMGHQLISHWLTHTAVLEPFIATHRHS 541
QY 560 VLHPHKLILVPHYKDTMTFINASAROVLTNANGLIETTHYPYSKYSMELSSILYKDWTFDQ 619
Db 542 VLHPHKLILHPRNTMINALARETL--TYDGGFTSLFPAPKYSMEMSAAYAKDWVFEQ 600
QY 620 ALPNMLKGLAVESSAPHLRLILINDYPPAVDGLDIWSAIKTWVQDYCCLYKDDNAV 679
Db 601 ALPADLLKRGVAVEDLSPPHGIRLLILDYPAVDGLLEIWAATKSWVTYCKFYKSDTV 660
QY 680 QNDFELOSWMNELREKHKHADKKHPEWPKMOTLSLIESCTTIWIASALHAAVNGQY 739
Db 661 EKDTLOAWKELREGEHGDCKDEAWNPKLQTRQELRDCCTIIWIASALHAAVFGYS 720
QY 740 YGGYILNRPRTTSRRFPEVGTATYKELESNPEKAFRTICSELOALVSIISIIILSKHAS 799
Db 721 YAGYLPNRPRTLSCLNMPBPSPGSEVEELKTNPKVFLKTFVPLQSLLSISIFEVSRHAS 780
QY 800 DEVYLGORASIDWTSKIALEAFKFGKKNLFEVENRIMERNEKVNKNSGPNVLYTL 859
Db 781 DEVYLGORDSIEWTKDKEPLVAFERFGKMLSDIENRIMMNSHKSKWKNRSGPNVLYTL 840
QY 860 VPSSNEGLTGRGIPNSISI 878
Db 841 FPTSSEGLTGKIPNSVSI 859

RESULT 8
T06339
lipoxigenase (EC 1.13.11.12) loxB - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T06339
R:Farrie, B.J.; Beaudoin, N.; Burkhardt, W.; Bowsher, C.G.; Rohstein, S.J.
Plant Physiol. 106, 109-118, 1994
A:Title: The cloning of two tomato lipoxigenase genes and their differential expression
A:Reference number: Z15612; MUID:95062736; PMID:7972514
A:Accession: T06339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-859 <PER>
A:Cross-references: EMBL:U09025; NID:9575431; PIDN:AAA3183.1; PID:9482901
A:Experimental source: strain Caruso; tissue-type fruit pericarp
C:Genetics:
A:Gene: loxB
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 60.2%; Score 2812.5; DB 2; Length 859;
Best Local Similarity 60.8%; Pred. No. 1.2e-183;
Matches 522; Conservative 141; Mismatches 185; Indels 11; Gaps 7;

QY 28 GNILDRVSSLGNN--KIKGVILMRNVLDFTFEHNLNDNFTLGGVSGVQLISATH 84
Db 4 GGIVDAI--LGKDRPKVKGKVLMMKNVLDFTINIGASVVDGSLDLGGVSGVQLISGV 61
QY 85 TSNDRGKGVGNKAYLERWLTISIPPLFAGESVFQINFQWD--ENFGPFGAFFIKNGHTSEFF 143
Db 62 NYDGLGKLSNPAYLESWLTIDITPITAGESTFSVTFDWRDEFQVPGAFIKNLHNEFF 121
QY 144 LKSLTLDDVPGYGRVHFDGNSWVPSGRYKDKRIFFANHVLPSTQNPPLRKYREELWN 203
Db 122 LKSLTLEDVPGYGRVHFDGNSWVPSGRYKDKRIFFANHVLPSTQNPPLRKYREELVA 181
QY 204 LRGGDTGERKEWDRIYDVYNDIADPDVGDH--RPILGGTTEYPYPRGRGRPRSRD 261
Db 182 LRGGDTGKLEWDVYACVNDLGECDKGEYARPIILGSGSEYFYPGRGRGREPTKAD 241
QY 262 HNYESRSPIMSLDIYVPKDNFGLKQSDPLGLVTLKALISIKPGLQSFIVPTNPFEDN 321
Db 242 PNCESRNPPLMSLDIYVPRDRFRGHVKKSDPLTSLKSLQTLPLFAFKALCDNTPEFNS 301

Db 848 PYMLYPNAGSDNSBSGLTGKIPNSVSI 876
RESULT 12
S01142
lipoxxygenase (EC 1.13.11.12) 3 [similarity] - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: S01142
R:Ealing, P.M.; Casey, R.
Biochem. J. 253, 915-918, 1988
A:Title: The complete amino acid sequence of a pea (Pisum sativum) seed lipoxxygenase protein
A:Reference number: S01142; MUID:89025643; PMID:3140791
A:Accession: S01142
A:Molecule type: mRNA
A:Residues: 1-861 <EAL>
A:Cross-references: EMBL:X07807; NID:g20799; PIDN:CAA30666.1; PID:g20800
C:Superfamily: lipoxxygenase
C:Keywords: oxidoreductase
Query Match 57.7%; Score 2696.5; DB 1; Length 861;
Best Local Similarity 58.3%; Pred. No. 9.8e-176;
Matches 506; Conservative 145; Mismatches 184; Indels 33; Gaps 7;
QY 30 ILDRVSSLGKNGKIKGVLMNSVLDFT-----EFHSLNDNFTELLGGVS 76
Db 8 ILNR-----GHKIKGVLMNRKVLNLSLTVGVGQGFIDLGSTVDNLTAFLGRSV 62
QY 77 FQLISATHTSDSRGKGVNKAYLERWLTSLIPPLFAGESVFOINPQWDFGFGAFPIKN 136
Db 63 LQLISATKPDATGKGLKATFLEGLISSLPTLCAGOSAPKIHFEWDDMGIPAFYIKN 122
QY 137 GHTSEFFLKSLLDVPYGVHVDGNSWYPSGRYKDRIFPANHVLPSQPNPLRKY 196
Db 123 FMOETFFLVSLDIPNHGSIYFCVNSWYNAKHKKIDRFANQYLYPSETPAPLVHY 182
QY 197 REELNLNRGDTGERKEWDRIYDVYNDIADPDVGDH--RPLIGGTETPYPRRGRTG 254
Db 193 REELNLNRGDTGERKEWRIYDVYNDLGNPDGSHARVVLGSEYIPYPRRGRTG 242
QY 255 RPRSRDNYESRLSPINSLDIYVPKDNFGHLKQSDPLGHTLKALISIKPLQSIPT-- 312
Db 243 RKPTRKDNSESR-----SDYVYLPDRDAFGLHKSDFLTLYGLKAVSQNVPALESVFFD 297
QY 313 -DVPNPEFNDKFNLDNLPFERGPIPPENAFKTLTDLTP-PLFKALVRNDGKELKPTPE 370
Db 298 LNFTNPEFDSFDEHGLYEGGIKLPN-----ILSQISPLPVKLEIFTDGENTLKYPFPK 353
QY 371 VYKDNKIOWSTDEBFARMLAGNPLLIIRLEAPPTSKLDPNVYGNQNSTITEEHKHG 430
Db 354 VIQVSRSGWMTDESFARMLAGVNPVICCLQEPFPRSKLDSQIYGDHTSKISKEHLEPN 413
QY 431 LDGLTVDEAMKONRLIYVDFDALMPYLTRMNATSTKYATRLTLKLDGDTAKPLVIEL 490
Db 414 LEGUTVEAIGKQLFLDDHDSIMPLYLRINSTKAYATRTLLFNNNQNLKPLAIEL 473
QY 491 ALPHPQGGQOLGAISKLFPFAENGQKSIQWLAKAYVTVDVGHQLISHWLTHAVLEPP 550
Db 474 SLPHPQGGDEHGAVSIVYQALLEGVSSIWLAKAYVINDSCYHQLVSHWLTHAVVEPP 533
QY 551 VIATHRQLSLVHPHTKLLVPHYKDTMTINASARQVLNANGLIETHTHPKYSWEISSIL 610
Db 534 VIATNRHLSLCHPIYKGLLYPHYRDTMINSLARLSLVNDGGIETKTLFWGRYSWEMSSKV 593
QY 611 YKDTFFPDQALPNMLKRGGLAVESDSSAPHLRLRLINDYPPAVDGLDTSWAIKTVQDYCC 670
Db 594 YKNWVFTQALPADLIRKGMALDEPSSPCGVKLVVEDYPPYAVDGLLEWAIKTVQDYVS 653
QY 671 LYYKDDNAVQNDPELQSWNELREKGHADKHEPWPMPQNTLSELIESCTTIWIASALH 730
Db 654 LYYTSDEKLRQDSLOQAWKELVGVGDKKNEPWPMPQNTREDLIEVCSIVITWIASALH 713
QY 731 AAVNFGQPYGGYILNRPTTSRRFMPVEVGTAEYKELESNPKEAPLRTICSELQALVSI 790

Db 714 AAVNFGQSYGGLILNRPTLSRRFMPKGSABFEELVKSQKAYLTKTPKFQTLIDLVS 773
QY 791 IEILSKHASDEVYLGORASIDWTSKIALAPEKEKGNLFVEINMERKEVNLKNSG 850
Db 774 IEILSRHASDELYLGERDNPNWTSKRALEAFKFGNKLAEIEKKLTQRNNDKURNRHG 833
QY 851 PYNLPYTLIAPSSNEGLTGRGIPNSISI 878
Db 834 PVEMPYTLIAPSSKEGLTFRGIPNSISI 861
RESULT 13
DASYLL
lipoxxygenase (EC 1.13.11.12) 2 - soybean
N:Alternate names: carotene oxidase 2; lipoxidase 2
C:Species: Glycine max (soybean)
C:Date: 31-Mar-1989 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001
C:Accession: A28161; A30831; A37160; S13536
R:Shibata, D.; Steczko, J.; Dixon, J.E.; Andrews, P.C.; Hermodson, M.; Axelrod, B.
J. Biol. Chem. 263, 6816-6821, 1988
A:Title: Primary structure of soybean lipoxxygenase L-2.
A:Reference number: A28161; MUID:88198254; PMID:2834391
A:Accession: A28161
A:Molecule type: mRNA
A:Residues: 1-865 <SHI>
A:Cross-references: GB:J03211; NID:gl70013; PIDN:AAA33987.1; PID:gl70014
A>Note: there are no disulfide bonds
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
Plant Mol. Biol. 7, 11-23, 1986
A:Title: Two soybean seed lipoxxygenase nulls accumulate reduced levels of lipoxxygenase
A:Reference number: A30831
A:Accession: A30831
A:Molecule type: mRNA
A:Residues: 232-262, 'NL', 265-312, 'Y', 314-362, 'E', 364-399, 'P', 401-427, 'H', 429-485, 'G', 487
A:Cross-references: GB:M16876
A:Experimental source: clone pLX-65
A>Note: due to a frameshift error, residues in the region 691-865 do not correspond to
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
unpublished results, cited by Yenofsky, R.L., Fine, M., and Liu, C., in Mol. Gen. Genet.
A:Reference number: A37160
A:Accession: A37160
A:Molecule type: mRNA
A:Residues: 232-312, 'Y', 314-399, 'PK', 402-427, 'H', 429-485, 'G', 487-501, 'G', 50
A>Note: this is a revision to the sequence from reference A30831
R:Shibata, D.; Kato, T.; Tanaka, K.
Plant Mol. Biol. 16, 353-359, 1991
A:Title: Nucleotide sequences of a soybean lipoxxygenase gene and the short intergenic re
A:Reference number: S13381; MUID:91370880; PMID:1909908
A:Accession: S13536
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 859-865 <SH2>
A:Cross-references: EMBL:X56139; NID:gl8745; PIDN:CAA33605.1; PID:g829267
C:Comment: In soybean, four isozymes are found with distinct electrophoretic properties.
C:Function:
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pen
C:Superfamily: lipoxxygenase
C:Keywords: fatty acid oxidation; iron: metalloprotein; oxidoreductase
F:527,533,718,722,865/Binding site: iron (His, His, His, Asn, Ile) #status predicted
Query Match 57.5%; Score 2690; DB 1; Length 865;
Best Local Similarity 58.4%; Pred. No. 2.8e-175;
Matches 513; Conservative 127; Mismatches 194; Indels 44; Gaps 8;
QY 23 VINAGNILDVSSIGGNKIKGVLMNSVLDFTFTH-----SNLL 64
Db 10 ILNR-----GGHKIKGVLMNRKVLNLSLTVGVGQGFIDLGSTLVNVGSL 59
QY 65 DNFTLGGGVFQLISATHTSDSRGKGVNKAYLERWLTSLIPPLFAGESVFOINPQWDF 124
Db 60 DNLTAFLGRSVALQLISATKPLANGKGVKXDTFLEGLISSLPTLCAGOSAFNIQFWE 119

R:Bunker, T.W.; Koetje, D.S.; Stephenson, L.C.; Creelman, R.A.; Mullet, J.E.; Grimes, H.
Plant Cell 7, 1319-1331, 1995
A:Title: Sink limitation induces the expression of multiple soybean vegetative lipoxigenase
A:Reference number: Z15673; MUID:96004535; PMID:7549487
A:Accession: T06429
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-859 <BUN>
A:Cross-references: EMBL:U26457; NID:G1262439; PIDN:AAA96817.1; PID:G1262440
A:Experimental source: cultivar Wye; leaf
C:Genetics:
A:Gene: vlxc
C:Function:
A:Description: catalyzes hydroperoxidation of polyunsaturated fatty acids containing a double bond
C:Superfamily: lipoxygenase
C:Keywords: iron; metalloprotein; oxidoreductase

Query Match 56.7%; Score 2649; DB 2; Length 859;
Best Local Similarity 58.0%; Pred. No. 1.7e-172; Mismatches 187; Indels 44; Gaps 8;
Matches 503; Conservative 133; Mismatches 187; Indels 44; Gaps 8;

QY 39 GNKIKGVILMSNYLDFTEPHS-----NLLDNFTLLGGG-----VS 76
DB 10 GQKIKGTVVLMPKNDLDFNAITSVGKGSADKATATDFLGKGLDALGHAVDALTAFAHSHS 69
QY 77 FQLISATHSNDGRKGVKNKAYLEWLTSIPPLFAGESVFOINFQWDENGFGGAFPIKN 136
DB 70 LQLISATQTDGSGKGVKNKAYLEKFLPTLPLGARQAFDINFEDASFGIPGAFYIKN 129
QY 137 GHTSEFFLKSLTLDVPVGYGRVHFPCNSWYPSGKYKDRIFFFANHVLPSPQENPLRKY 196
DB 130 FMTDEFFLVSKLEDPNHEGINFVCSWVNFKSKYKRRIFVNDYVLPSPATFGLVY 189
QY 197 REELWNI RGDTGTERKWDRIYDVYNDADPDVGDHRLPILGTTTEYYPRRGRTRP 256
DB 190 RQEELEVLRGDTGTRKRRDFRIYDIYNDLGNPDGDPRIIGSSSNYPYPRVRTGRE 249
QY 257 RSRDRHNYESRLSPIMSIDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLOSI---FD 313
DB 250 KTRKDPNSEK-----PGEIYVPRDENFGLKSSDFLTGYKISLSONVPLFKSIIILNR 303
QY 314 VTPNFDNFKVDNLFERGFPIPNFAKTLTDLTP-PLFKALVRNDGEXFLKPPTEPVV 372
DB 304 VTSSEFDSFDEVRGLFEGGIKLPTN-----ILSQISPLPLVKEIFRTDGTENTLQPPPHVI 359
QY 373 KDNKIGWSTDEFAREMLAGNPLLIRELEAPPTSKLDPNVYGNQNSTITEHKKGLD 432
DB 360 RVSKSGWMTDEFAREMLAGNPNVIRLQEPFPKSLDPAITYGDTSTITKQOLEINLG 419
QY 433 GLTVDEAMKQRLXIVDFHDALMPYLTRMNAIS-TKTYATRTLLLLKDDGTLKPLVIELA 491
DB 420 GVTVEEALSAHRLFLDYHDFAFFPYLTAKAYATRTILFKDDGSLKPLAIELS 479
QY 492 LPHPCGDQDGAISKLYPFAENGQVKSIMQAKAYVTVNDVYHQLISHNLHTHVALEPFV 551
DB 480 KP-----ATVSKVVLPALEGVESTLWLLAKAHVIVNDGYHQLISHNLHTHVALEPFA 532
QY 552 IATHRLQSLVHLPIHKLIVPHYKDMFMFNASARQVLINANGLIETHYPSKYSMELSSILY 611
DB 533 IATNRHLSVLHPIYKLLVPHYKDMININGLARQSLINAGGIIETFLPGKYSIEMSSVY 592
QY 612 KDWTFPDQALPNLMLKRGIAVEDSAPHGLRLINDYPPFAVDGLDIMSALIKTWVQDYCCL 671
DB 593 KXWVFTDQALPADLVKRGIAVEDSAPHGLRLVIEDYPYAVDGLIEWDAIKTWVHEYSV 652
QY 672 YYKDDNAVQNDPELQSWNNEUREKHADKKHPPWPKMQLSELIESCTTIIWIASALHA 731
DB 653 YYPITNAALQQDTELAQAWKEVVEKGGHGLDKDPWPKLQTVEDLIQSCSIIWIASALHA 712
QY 732 AVNFGQYPIGGYIILNRPITISRRFMPEVGTABYKELESNPKAFURITCSELQALVISII 791
DB 713 AVNFGQYPIGGYIILNRPITISRRFMPEVGTABYKELESNPKAFURITCSELQALVISII 772

QY 792 EILSKHASDEVYLGQRASIDWTSKIALEAFKFGKLNLFVEVNRIMERKEVNLKNRSGP 851
DB 773 EILSRHASDEVYLGQRDNPNWTTDSKALEAFKFGKLNLFVEVNRIMERKEVNLKNRSGP 832
QY 852 VNLPTYLLVPSSNEGILTRGIPNSISI 878
DB 833 VQLPYTLHRSSEEGMSFKGIPNSISI 859

Search completed: July 16, 2004, 12:03:55
Job time : 43.0332 secs

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OM protein - protein search, using sw model

Run on: July 16, 2004, 11:30:53 ; Search time 167.411 Seconds
(without alignments)
1481.839 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675
Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVPSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4675	100.0	878	4 AAB11500	C. sativu
2	4675	100.0	878	4 AAB86036	Cucumber
3	3933	84.1	880	6 AAO27492	Balsam pe
4	3011.5	64.4	859	6 ABO19443	Wine grap
5	2995.5	64.1	862	6 ABO19442	Wine grap
6	2992.5	64.0	857	4 AAB46803	Potato LO
7	2911	62.3	862	6 ABP70404	Amino aci
8	2791	59.7	857	5 ABG30570	Glycine m
9	2690	57.5	865	5 ABG30569	Glycine m
10	2639.5	56.5	864	2 AAR24042	Lipoxigen
11	2591	55.4	853	2 AAR50220	Soybean l
12	2582.5	55.2	839	5 ABG30568	Glycine m
13	2502	53.5	863	7 ADC53139	9'-specif
14	2439.5	52.2	837	6 ADA48504	Rice prot
15	2438	52.1	862	5 AAU99691	Barley wi
16	2438	52.0	862	5 ABG30566	Wild type
17	2431	52.0	862	5 AAU99693	Barley wi
18	2431	52.0	862	5 AAU99692	Barley wi
19	2431	52.0	862	5 ABG30567	Mutant ty
20	2424	51.9	864	5 ABG30571	Barley lo
21	2423.5	51.8	887	6 AAO27494	Corn (Zea
22	2390.5	51.1	865	2 AAR23797	Rice lipo
23	2390.5	51.1	865	2 AAR20670	Lipoxigen
24	1845	39.5	491	7 AAE39891	Human lip
25	1705.5	36.5	924	6 AAE38266	Rice dise

26	1656	35.4	923	2 AAR61136	Aar61136 Plant bli
27	1653	35.4	901	4 AAY97741	Aay97741 H. annus
28	1628	34.8	445	6 AAO27493	Aao27493 Garden ba
29	1498.5	32.1	922	5 AAU76150	Aau76150 Rice lipo
30	1316	28.1	244	4 AAB86035	Aab86035 Cucumber
31	790	16.9	301	3 AAG24811	Aag24811 Arabidops
32	773.5	16.5	464	6 AAO27495	Aao27495 Corn (Zea
33	722	15.4	312	3 AAG23228	Aag23228 Arabidops
34	706.5	15.1	222	4 AAG83338	Aag83338 P patens
35	706.5	15.1	222	4 AAG80888	Aag80888 Lipid deg
36	674.5	14.4	170	6 AAO27487	Balsam pe
37	552	11.8	240	3 AAG23230	Arabidops
38	546.5	11.7	193	3 AAG24812	Arabidops
39	546.5	11.7	242	3 AAG23229	Arabidops
40	516.5	11.0	663	5 AAE15433	Human 5-1
41	516.5	11.0	674	1 AAP90730	Synthetic
42	516.5	11.0	674	5 AAE15432	Human 5-1
43	516.5	11.0	674	6 ABU08713	Alzheimer
44	516.5	11.0	674	6 ABU89732	Protein d
45	516.5	11.0	674	6 ABR42216	Mouse CAS

ALIGNMENTS

RESULT 1

AAB11500
ID AAB11500 standard; protein; 878 AA.

XX AC AAB11500;

DT 13-MAR-2001 (first entry)

XX C. sativu LOX protein.

XX LOX; lipoxigenase; cucumber; plant; 6-hydroperoxy-gamma-linolenic acid;

KW 9-hydroperoxy-gamma-linolenic acid; 6,9-hydroperoxy-gamma-linolenic acid;
KW gamma-linolenic acid.

XX Cucumis sativu.

XX DE19914464-AL.

XX 05-OCT-2000.

XX 30-MAR-1999; 99DE-01014464.

XX 30-MAR-1999; 99DE-01014464.

XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.

XX Feussner I, Hornung E;

XX WPI; 2001-103874/12.

XX Preparation of plant lipoxigenase with altered position specificity
XX comprises replacing at least one amino acid in the wild type lipoxigenase
XX amino acid sequence.
XX Disclosure; Fig 5; 14pp; German.
XX This invention describes a novel preparation of plant lipoxigenase (I)
XX with altered position specificity which comprises replacing at least 1
XX amino acid in the wild type lipoxigenase amino acid sequence. The method
XX also describes (1) (I) prepared by the method above; (2) nucleic acid
XX encoding (I); (3) a vector comprising the nucleic acid of (2); (4) a cell
XX comprising the vector of (3); (5) a plant or plant part comprising a host
XX cell as in (4); (6) preparation of 6-, 9- and/or 6,9-hydroperoxy-gamma-
XX linolenic acid comprising reacting gamma-linolenic acid with (I); and (7)
XX a gamma-linolenic acid derivative comprising a hydroperoxy group or a
XX hydroxy group at position 6

XX Sequence 878 AA;

Query Match	100.0%;	Score 4675;	DB 4;	Length 878;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 878;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGNGIKGKVIILMRSNVLDFTTEFH	60	
Db	1	MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGNGIKGKVIILMRSNVLDFTTEFH	60	
QY	61	SNLLDNFTTELLGGVVSFOLISATHTSNDGRGVGNKAYLERWLTSPPLFAGESVFQINF	120	
Db	61	SNLLDNFTTELLGGVVSFOLISATHTSNDGRGVGNKAYLERWLTSPPLFAGESVFQINF	120	
QY	121	QNDENFGPGAFPIKNGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWVPSGYKKDRIFFA	180	
Db	121	QNDENFGPGAFPIKNGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWVPSGYKKDRIFFA	180	
QY	181	NHVYLPSTQPNLRKYREEELWNLRGDGTGERKEWDRIYDYVDVNDIADPDVGDHRPILG	240	
Db	181	NHVYLPSTQPNLRKYREEELWNLRGDGTGERKEWDRIYDYVDVNDIADPDVGDHRPILG	240	
QY	241	GTEYYPFRGRTGPRSRDRHNYESRLSPIMSLDIYVPKDNFGHLKMSDFLGYTLKAL	300	
Db	241	GTEYYPFRGRTGPRSRDRHNYESRLSPIMSLDIYVPKDNFGHLKMSDFLGYTLKAL	300	
QY	301	SISIKPGLQSIQFDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTEDLTPPLFKALVRNDG	360	
Db	301	SISIKPGLQSIQFDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTEDLTPPLFKALVRNDG	360	
QY	361	EKFLKFPTEPVVKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS	420	
Db	361	EKFLKFPTEPVVKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS	420	
QY	421	TITEEHIKHGLDGLTVDEAMKQNRLYIVDFHDLMPYLTRMNAVSTKTYATRTLLKDD	480	
Db	421	TITEEHIKHGLDGLTVDEAMKQNRLYIVDFHDLMPYLTRMNAVSTKTYATRTLLKDD	480	
QY	481	GTLPKPLVIELALPHQGGOLGAIKLYPPAENGVOKSIWQAKAYVTVDVGHOLISHW	540	
Db	481	GTLPKPLVIELALPHQGGOLGAIKLYPPAENGVOKSIWQAKAYVTVDVGHOLISHW	540	
QY	541	LHTHAVLEPFFVIATHRQLSVLHPHKLAVPHYKDTMFINASARQVLINANGLIBETHYPS	600	
Db	541	LHTHAVLEPFFVIATHRQLSVLHPHKLAVPHYKDTMFINASARQVLINANGLIBETHYPS	600	
QY	601	KYSMELSSILYKQWTFPQOALPNMLMKGLAVERSSAPHGRLILINDYPPAVDGLDWSA	660	
Db	601	KYSMELSSILYKQWTFPQOALPNMLMKGLAVERSSAPHGRLILINDYPPAVDGLDWSA	660	
QY	661	IKTWYQDYCCLYYKDDNAVQNDFFELQSWWNLREKGHADKKHEPWPQWQTLSELIESCT	720	
Db	661	IKTWYQDYCCLYYKDDNAVQNDFFELQSWWNLREKGHADKKHEPWPQWQTLSELIESCT	720	
QY	721	TIITWASALHAANFGQPYGGYILNRTTERRRPMVEGTAIEYKELSENPEKAPLRTICS	780	
Db	721	TIITWASALHAANFGQPYGGYILNRTTERRRPMVEGTAIEYKELSENPEKAPLRTICS	780	
QY	781	ELQALVSIISIIELSKHASDEVILGORASIDWTSKIALAEFAFEFGKQLFEVENRIMERN	840	
Db	781	ELQALVSIISIIELSKHASDEVILGORASIDWTSKIALAEFAFEFGKQLFEVENRIMERN	840	
QY	841	KEVNLKRSQPNVLPYTLVSSNEGLTGRGIPNSISI	878	
Db	841	KEVNLKRSQPNVLPYTLVSSNEGLTGRGIPNSISI	878	
RESULT 2				
AAB86036				
ID	AAB86036	standard; protein; 878 AA.		
XX				
AC	AAB86036;			
XX				
DT	13-JUL-2001	(first entry)		

XX DE Cucurbit LBLOX protein SEQ ID 4.
XX KW Cucurbit; LBLOX; fatty acid metabolism; lipid metabolism;
XX KW plant oil-production; transgenic plant.
XX OS Cucumis sativus.
XX PN DE19950921-A1.
XX PD 26-APR-2001.
XX PF 21-OCT-1999; 99DE-01050921.
XX PR 21-OCT-1999; 99DE-01050921.
XX PA (BADI) BASF AG.
XX PI Kindl H, May C, Feussner I;
XX DR WPI; 2001-274658/29.
XX DR N-PSDB; AAF88022.
XX PT New isolated nucleic acid encoding sequence that targets proteins to
XX PT lipid bodies, useful for producing transgenic plants for lipid and fatty
XX PS acid production.
XX PS Disclosure; Page 18-21; 30pp; German.
XX CC This invention describes a novel isolated nucleic acid sequence (I),
XX CC encoding a polypeptide, comprising a sequence (Ia) involved in fatty acid
XX CC or lipid metabolism, and a targeting sequence (Ib). (I) are used to
XX CC produce oil-producing transgenic plants or eukaryotic microorganisms, for
XX CC production of lipids or derived fatty acids. This sequence represents a
XX CC Cucumis sativus (cucumber) LBLOX protein which is described in the method
XX CC of the invention
SQ Sequence 878 AA;
Query Match 100.0%; Score 4675; DB 4; Length 878;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 TITEHIKGLDGLTVDEAMKQNLVYVDFHDLMPYLTRMNTATSTKYATRILLKDD 480
 Qy 481 GTLKPLVIELALPHPQGDQLGAIKSLYFPAENGQKSIWOLAKAYVTVDVGHQLISHW 540
 Db 481 GTLKPLVIELALPHPQGDQLGAIKSLYFPAENGQKSIWOLAKAYVTVDVGHQLISHW 540
 Qy 541 LHTHAVLEPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINAGLIETTHYS 600
 Db 541 LHTHAVLEPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINAGLIETTHYS 600
 Qy 601 KYSMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVDGLDWSA 660
 Db 601 KYSMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVDGLDWSA 660
 Qy 661 IKTWQDYCCLYYKDDNAVQNDPFLQSWNLEKRGHAKKHBPWPMPQOTLSELBSCT 720
 Db 661 IKTWQDYCCLYYKDDNAVQNDPFLQSWNLEKRGHAKKHBPWPMPQOTLSELBSCT 720
 Qy 721 TIWIASALHAANFGQYPYGGYILNRPPTTSRRPMPVEGTAAYKELESNPEKAFRLTICS 780
 Db 721 TIWIASALHAANFGQYPYGGYILNRPPTTSRRPMPVEGTAAYKELESNPEKAFRLTICS 780
 Qy 781 ELQALVSIISIEILSKHASDEVYLGQRASIDWTSKIALFAFEKFGKQLFEVENRIMERN 840
 Db 781 ELQALVSIISIEILSKHASDEVYLGQRASIDWTSKIALFAFEKFGKQLFEVENRIMERN 840
 Qy 841 KEVNLKNSRSGPNLPYTLVPSNNEGLTGRGIPNSISI 878
 Db 841 KEVNLKNSRSGPNLPYTLVPSNNEGLTGRGIPNSISI 878

RESULT 3
 AAO27492
 ID AAO27492 standard; protein; 880 AA.
 AC AAO27492;
 DT 06-NOV-2003 (first entry)
 DE Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.
 KW Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;
 KW fatty acid metabolite synthesis; signal molecule; growth regulation;
 KW development regulation; plant development; wound response;
 KW genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.
 OS Momordica charantia.
 XX US2003074593-A1.
 XX 17-APR-2003.
 XX 29-JAN-2002; 2002US-00059909.
 XX 10-FEB-1999; 99US-0119597P.
 XX 09-FEB-2000; 2000US-00501422.
 XX (CAHO/) CAHOON E B.
 XX (KINN/) KINNEY A J.
 XX (KLEI/) KLEIN T M.
 XX (LEEJ/) LEE J.
 XX (PEAR/) PEARLSTEIN R W.
 XX (RAFA/) RAFALSKI J A.
 XX (SHEN/) SHEN J B.
 XX (THOR/) THORPE C J.
 XX (TING/) TINGEY S V.
 XX (WENG/) WENG Z.
 XX Caboon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;
 XX Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;
 XX WPI; 2003-567325/53.
 XX N-PSDB; AAL57712.

XX New isolated polynucleotides encoding plant lipoxigenases, useful in
 PT genetic mapping, particularly in catalyzing hyperoxidation of
 PT polyunsaturated fatty acids.
 XX Claim 19; Page 23-25; 36pp; English.
 XX This invention relates to novel nucleotide sequences which encode
 CC proteins which have lipoxigenase activity. Lipoxigenases are membrane
 CC bound ubiquitous enzymes which catalyze the hydroperoxidation of
 CC polyunsaturated fatty acids in the first step of fatty acid metabolite
 CC synthesis. Products of this pathway are found as signal molecules
 CC involved in growth and development regulation. A knowledge of the amino
 CC acid sequence of lipoxigenases may allow the understanding of plant
 CC development and wound response. The polynucleotides, polypeptides and
 CC lipoxigenases of the invention may therefore be useful in genetic mapping
 CC and particularly for catalyzing hydroperoxidation of polyunsaturated
 CC fatty acids. The present sequence is the amino acid sequence of the
 CC Balsam pear (Momordica charantia) lipoxigenase protein 2 of the invention
 XX Sequence 880 AA;
 SQ

Query Match 84.1%; Score 3933; DB 6; Length 880;
 Best Local Similarity 81.7%; Pred. No. 0;
 Matches 719; Conservative 83; Mismatches 76; Indels 2; Gaps 1;

Qy 1 MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGSKNKIKGVILMRSNVLDTFFH 60
 Db 1 MFGIGKSIIEGAVNTTGDLAGSVINAGNIVGRVNTIGGKTKGVVILMRSNVLDTFFH 60
 Qy 61 SNLDNFTLGGGVSFQLISATHTSNDNRGKVGKAYLERWLTSIFPLFAGESVFQINF 120
 Db 61 SSLDGVTELLGGGISLQLISATHASNDNRGKVGKAFLEWLTSVPLFAGESVFQVNF 120
 Qy 121 QWDENFGFGAPFIKNGHTSEFFLSKSLDLDVPGYGRVHFDGNSVYSGRKKDRIEPA 180
 Db 121 DWEENFGFGAPFIKNGHTSEFFLSKSLDLDVPGYGRVHFDGNSVYSGRKKDRIEPA 180
 Qy 181 NHVYLPQSTQPNLRKYRBEELNLRGDTGKGEKWDRIYDVYNDIADPDVGDH--RPI 238
 Db 181 NHTCLPIDTDSLRYRBEELNLRGDTGKGEKWDRIYDVYNDLCDPNGGPNLVAPI 240
 Qy 239 LGGTEYYPRRGRTGRPRSRDHYESRLSPIMSLDIYVPKDNFGLKXSDFLGYTLK 298
 Db 241 LGGSDQYPYRRGRTGRPPARKDHYESRLSDVMSLNIYVPRDENFGLKXADFLGTLK 300
 Qy 299 ALSISIKPGLQSIEDVTNPFNPFNKEVDNLRERGPPIPNAPFKTLTDLTPPLFKALVN 358
 Db 301 VLSTSIQGLSIFDSTPGCFKFEVDLPERGPPIPLNFKNTEDLAPPLFKALVS 360
 Qy 359 DGEKFLKFTPEVVKDNKIGWSTDEFAPEMLAGNPLLRLEAPPTSKLDPNVYGNQ 418
 Db 361 DGERFLKYPTQVVKDNKLGWRTDEFAPEMLAGNPLIIRLEVEFPLSKLDPHVYGNQ 420
 Qy 419 NSTITTEHIKGLDGLTVDEAMKQNLVYVDFHDLMPYLTRMNTATSTKYATRILLK 478
 Db 421 NSTMTTEEQIKHGLDGLTVDEAKENKLYILDHHDAMPYLRINISTKTATRILLFLK 480
 Qy 479 DDGTLKPLVIELALPHPQGDQLGAIKSLYFPAENGQKSIWOLAKAYVTVDVGHQLIS 538
 Db 481 DDSTLKPLAIELSLPHPQGDDEHGAISKLYFPAEGRVESAIWOLAKAYVAVNDGYHQLNS 540
 Qy 539 HMLHTHAVLEPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINAGLIETTHY 598
 Db 541 HMLHTHAVLEPFVITTHRLSVLHPHKLIVPHYKDTMETINASARQVLINAGLIETTHY 600
 Qy 599 PSKYSMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVDGLDIW 658
 Db 601 PAKYAMELSSYIKYKWKFPDEALPTNLIKRGVAIEDSGSPHGVRLINDYPFAVDGLETW 660
 Qy 659 SAIKTVWQDYCCLYYKDDNAVQNDPFLQSWNLEKRGHAKKHBPWPMPQOTLSELBS 718
 Db 661 SAIKTVWTDYCSLYYKDDAIRNDVLEQSWNLEKRGHAKKHBPWPMPQOTLSELBS 720

ID	ABO19442	standard; protein; 862 AA.	
XX	AC	ABO19442;	
XX	DT	27-AUG-2003. (first entry)	
XX	DE	Wine grape lipoxigenase LOX1.	
XX	KW	Wine grape; lipoxigenase; LOX; flavour; fermented beverage; enzyme;	
XX	KW	grape juice; cheese; yogurt; pickle; tissue specificity; timing; wine.	
XX	OS	Vitis vinifera.	
XX	PN	US2003033627-A1.	
XX	PD	13-FEB-2003.	
XX	PF	16-OCT-2001; 2001US-00978522.	
XX	FX	16-OCT-2000; 2000US-0241220P.	
XX	PA	(DESC/) DESCENZO R A.	
XX	PA	(IREL/) IRELAN N A.	
XX	PI	Descenzo RA, Irelan NA;	
XX	DR	WPI; 2003-492095/46.	
XX	DR	N-PSDB; ACD28851.	
XX	PT	Novel purified and isolated Vitis vinifera lipoxigenase polypeptide,	
XX	PT	useful for modifying the flavor of a comestible e.g., a beverage which is	
XX	PT	a fermentation product, preferably wine.	
XX	PS	Claim 7; Page 14; 36pp; English.	
XX	CC	The invention relates to a purified and isolated Vitis vinifera	
XX	CC	lipoxigenase (LOX) polypeptide. The polypeptide is useful for modifying	
XX	CC	the flavour of a comestible e.g. a beverage which is a fermentation	
XX	CC	product, preferably wine. The polypeptide is useful for analysing the	
XX	CC	effect of LOX polypeptides on flavour production in wine and grape juice.	
XX	CC	The polypeptide is useful in the production of cheese, yogurt, pickles	
XX	CC	etc. The polypeptide is also useful in screening assays to identify	
XX	CC	modulators that modulate the activity of the Vitis vinifera LOX	
XX	CC	polypeptides. The polynucleotide is useful in heterologous production of	
XX	CC	pure lipoxigenase enzyme in a protein expression vector and for studying	
XX	CC	the native level of gene expression in response to environmental or	
XX	CC	viticultural influences. The cloned gene can be used to produce	
XX	CC	transgenic plants to modify the level of gene expression to produce	
XX	CC	optimal levels of lipoxigenase in the grape. Knowledge of Vitis vinifera	
XX	CC	lipoxigenase coding DNA sequences allows for modification of cells to	
XX	CC	permit, increase or decrease, expression of endogenous Vitis vinifera	
XX	CC	lipoxigenase. Such knowledge also permits modification of timing and	
XX	CC	tissue specificity of LOX expression. The DNA sequence information also	
XX	CC	makes possible the development through, e.g. homologous recombination or	
XX	CC	knock-out strategies of grapes that fail to express functional	
XX	CC	lipoxigenase or that express a variant of Vitis vinifera lipoxigenase.	
XX	CC	Such plants are useful as models for studying the in vivo activities of	
XX	CC	Vitis vinifera lipoxigenase and modulators of Vitis vinifera	
XX	CC	lipoxigenase. The present sequence represents the amino acid sequence of	
XX	CC	a wine grape lipoxigenase LOX	
XX	SQ	Sequence 862 AA;	
	Query Match	64.1%; Score 2995.5; DB 6; Length 862;	
	Best Local Similarity	63.6%; Pred. No. 8.2e-263;	
	Matches 546;	Conservative 134; Mismatches 169; Indels 9; Gaps 4;	
QY	30	ILDRVSSLG---NKIKGVILNRSNVLDTEFHSNLLDNFTLLGGVSGFQLISATH- 84	
DB	5	LLSIVSAITGNDKKEGTVLVMKKNVLDNFNDNAPVRDRVHFLFGQVSLQVLSAVHG 64	
QY	85	-TSNDSRGKVGKNKAYLEWLTLSIPLFAGESVFOINFOWDENFGPFAFKNGHTSEFF 143	

Db	65	DPANGLOGLKGRPAYLEDWITITSLTAGESAFKVTDFDWEDEIGEPGAFIIRNNHSEFF 124
QY	144	LKSLTLDDVPGYGRVHFCNSWVPSGKYKDDRIFFANHVLPSTPNPLRKYREEELWN 203
Db	125	LRTILFEDVPGGRHIFVCSNWSYPAKYKTDVFTQTVLPSTPGPLRKYRGELVN 184
QY	204	LRGDTGERKWDRIYDYVNDIADP--DVGDHPIILGGTTEYPPRRGTRPRSRD 261
Db	185	LRGDTGELKWDRIYDYVNDIADP--DVGDHPIILGGTTEYPPRRGTRPRSRD 244
QY	262	HNYESRLSPMSLDIYVPCDENFGLKMSDFGLVTLKALSISIKPGLSIEDVTNEPDN 321
Db	245	PXTESKPLVMSLNIYVPRDERFGLKMSDFGLVTLKALSISIKPGLSIEDVTNEPDN 304
QY	322	FKEVDNLFERGFPIFNFAFKTLTLP--PLFKALVRNDGEKFLKFPTEPVVKNKIGWS 380
Db	305	FQDVLIDYEGGIKVPPEGLDDKIKNIPLEMLKELVRTDGEHLKFPMPQVVKEDKSAWR 364
QY	381	TDEEFAREMLAGPNLLIRLEAFPTSKLDNVTYGNQNSITTEBHIKHGLDGLTVDEAM 440
Db	365	TDEEFAREMLAGPNVIRLLQEPFKSLDPEVYGNQNSITTEBHIKHGLDGLTVDEAM 424
QY	441	KONRLYIVDFHDLMPYLTRMNATSTKTATVATLTLKDDGTLKPLVIELALPHPGQQL 500
Db	425	EKKRFLDHDHDFVPEYLERINTTSTKYASRTLLFLKDDGTLKPLVIELALPHPGQQL 484
QY	501	GAISKLYFPAENGVOKSIWOLAKAVVYVNDVGYHOLIISHLWTHAVLPFVIATHRQLSV 560
Db	485	GAIVKYVTPAEDGVEGSIWOLAKAVVYVNDVGYHOLIISHLWTHAVLPFVIATHRQLSV 544
QY	561	LPIPHKLLVPHVKDWMFNASARVLIINAGLIETHYPSKYSMELSSITLYKDWTFPQQA 620
Db	545	LPIPHKLLVPHVFDVFNALARQILINAGGVVESTVFPKYSMESSVYKDWLTQQA 604
QY	621	LPNNLMKRGVAVDSAPHLRLINDYFVAVDGLDIWSAINTWYDCCLYYKDDNAVQ 680
Db	605	LPADLIKRGVAVDSAPHLRLINDYFVAVDGLDIWSAINTWYDCCLYYKDDNAVQ 664
QY	681	NPELQSWNLEKRECHADKHEPWPVKOTLSIELCTTIITIASALHAHVNGQVPPY 740
Db	665	KDSELSQSWNLEKRECHADKHEPWPVKOTLSIELCTTIITIASALHAHVNGQVPPY 724
QY	741	GGYILNRPITTSRRFPEVGTAEYKELESNPEKAFRTICSELQALVSIISIEILSKHSD 800
Db	725	AGVLPNRPITTSRRFPEVGTAEYKELESNPEKAFRTICSELQALVSIISIEILSKHSD 784
QY	801	EYVLGRASIDVTSKIALEAFKGLFEVFNEMERNKEVNIKNRSGPVNLYPTLLV 860
Db	785	EYVLGRASIDVTSKIALEAFKGLFEVFNEMERNKEVNIKNRSGPVNLYPTLLV 844
QY	861	PSNEGLTGKGPNSISI 878
Db	845	PTSEGLTGKGPNSIVI 862
	RESULT 6	
	AAB46803	
ID	AAB46803	standard; protein; 857 AA.
XX	AC	AAB46803;
XX	DT	23-APR-2001 (first entry)
XX	DE	Potato LOX protein.
XX	KW	Potato; LOX protein; lipoxigenase; arachidonic acid; mutant; plant;
XX	KW	11-arachidonate-lipoxigenase; 11-hydroperoxy-arachidonic acid.
XX	OS	Solanum tuberosum.
XX	PN	WO2001043223-A2.
XX	FX	18-JAN-2001.

XX PF 10-JUL-2000; 2000WO-EP006539.
 XX PR 08-JUL-1999; 99DE-01031819.
 XX PA (IPBP-) IPB INST PFLANZENBIOCHEMIE.
 XX PI Feussner I, Hornung E, Rosahl S;
 XX DR WPI; 2001-081054/09.
 XX PT New nucleic acid encoding lipoxigenase useful for producing 11-
 XX PT hydroperoxy- or hydroxy-arachidonic acid.
 XX PS Disclosure; Fig 3; 18pp; German.
 XX CC This invention describes a novel nucleic acid (I) encoding a potato
 CC lipoxigenase protein, LOX, (II) is new. The invention also describes (1)
 CC (III), a sequence of 857 amino acids (aa), given in the specification; (2)
 CC a vector (III) comprising (I); (3) a host cell (IV) comprising (I) or
 CC (III); (4) a plant or part of a plant comprising (IV); (5) enhancing the
 CC specificity of a plant lipoxigenase for position 11 of arachidonic acid;
 CC comprising mutating at least one amino acid of the wild type lipoxigenase;
 CC (6) producing 11-hydroperoxy-arachidonic acid or the reduced 11-hydroxy-
 CC derivative comprises treating arachidonic acid with (II) and further
 CC reducing the obtained hydroperoxy form to the hydroxy form; (7) the
 CC arachidonic acid derivative, comprising a hydroperoxy group or a hydroxy
 CC group at position 11. (II) is useful for producing 11- hydroperoxy-
 CC and/or 11-hydroxy-arachidonic acid. The lipoxigenase is specific for
 CC position 11 of arachidonic acid
 XX SQ Sequence 857 AA;

Query Match 64.0%; Score 2992.5; DB 4; Length 857;
 Best Local Similarity 64.9%; Pred. No. 1.5e-262;
 Matches 552; Conservative 123; Mismatches 167; Indels 9; Gaps 4;

QY 37 LGGN---KIKGKVLMSNVLDTEFHNSLLDNFTLLGGVSGFQLISATHT--SNDSR 90
 DB 7 IGGHDSKKVGTVMKKNALDFTDLGSLTDKIFALGQKVSFQLISSVQSPANGLQ 66
 QY 91 GKVGKAYLERWLTISPLPAGESVFQINQWENFGFPAGFFIKNGHTSEFFLKSLTLD 150
 DB 67 GKHSNPAYLENFLTLLAAGETAFTGVTFDWNESEFGVPGAFIKNTHINEFFLKSLTLE 126
 QY 151 DVPQYGRVHFDCNSWVPSGKYKDRIFFAHNVLPSTQNPPLKRYEELWNLRGDGTG 210
 DB 127 DVFNHGKVFHVCNSWVPSFRYKSDRIFFANQPLPSTPELLKRYENELLTURGDTG 186
 QY 211 ERKEWDRIYDVYNDIADPPVGDH--RPILGGTTEYPYPRGRGTGRPRSRDHNYESRL 268
 DB 187 KREAMDRIYDVYNDLGNPDQGEQNVRTLLGGSADYPPRGRGTGRPTRTDPKSESRI 246
 QY 269 SPMSLDIYVPKDNFGLKMSDFLGYTLKALSIKPGLOSIFDVTNPFDFKVDNL 328
 DB 247 PULISLDIYVPRDERFGLKMSDFLTALKSIVQIFLPELHALDGTNPEDSPEDVRL 306
 QY 329 FERGFPIPFN-AFKTLTDLTPPLFKALVRNDGKFLKFTPEVVKDKNGKWSDEEFAR 387
 DB 307 YEGGIKLQGGPLFKALTAAPLEMMKELLRTDGEGLRFFPTPLVIKSKTAWRTDESFAR 366
 QY 388 EMLAGNELLIRLEAPPTKLDPNVGNQNSITTEHIIKHGLDGLTVDAMKQNELYI 447
 DB 367 EMLAGNPIIISRLQEFPPKSLDPEAYGNQNSITTAETHIEDKLDGLTVDAMNNKLF 426
 QY 448 VDFHALMPYLTRMATSTKYATVATLLKDDGTLKPLVLTELAPHPQGDOLGAISKLY 507
 DB 427 LNHHDVLPYLRINRTTKYVASTLLFLQDNGSLKFLALIELSLPHPDGQDFVISKVY 486
 QY 508 PFAENGQKSIQWLAKAYVTVNDVGVHQLISHWLTHTAVLEFPFVIATHRQLSLVHPHKL 567
 DB 487 TPSDQGVESVSIQWLAKAYVAVNDVSGVHQLISHWLTHTAVIEFPFVIATHRQLSLVHPHKL 546

QY 568 LVPHYKDTMFINASARQVLINANGLIETHYPSKYSMELSSILYKDWTFPDQALFNNLMK 627
 DB 547 LYPHFEDTWNINAMARQILINAGGVLESTVFPFKFAMEMSAVVYKDWTFPDQALPADLVK 606
 QY 628 RGLAVEDSSAPHLRLINDYFPAVDGLDINSATKVTQDYCCLYYKDDNAVONDFELOS 687
 DB 607 RGVAVEDSSSPGVRLLIEDYFPAVDGLEINSATKSVTDYCSFYGSDEILKDKNELOA 666
 QY 688 WNNELREKGHADKKHEPMPKMTLSLIESCTTIWIASALHAAVNFGQYPPGGYILNR 747
 DB 667 WKELREVGCHGDKNEPMPMETPQELIDSTTIWIASALHAAVNFGQYPPAGYLPNR 726
 QY 748 PTTSRFMPVGTABYKELSNPEKAFRTICSELOALVSIISIIILSKHASDEVYLQOR 807
 DB 727 PTVSRFMPVGTPEYELKKNPKAFKLTITAQTLTLLGSLIELSRHTTDEIYLQOR 786
 QY 808 ASIDWTSKIALAEFEKFGKNLFEVENRIMENKVNKLKRSQPNVLPVTLVPSSEGL 867
 DB 787 ESEWTKDEPLAARFKGKLTIDIEKLIQRNGNLTNRSGPVNAPYTLFFPTESEGL 846
 QY 868 TCRGIPNSISI 878
 DB 847 TKGIPNSVSI 857

RESULT 7
 ABP70404
 ID ABP70404 standard; protein; 862 AA.
 XX AC ABP70404;
 XX DT 07-APR-2003 (first entry)
 XX DE Amino acid sequence of tobacco lipoxigenase-1 (LOX-1).
 XX KW Lipoxigenase-1; LOX-1; enzyme; plant; dioxygenation;
 KW polynaturated fatty acid; pentadiene; disease resistance; Solanacea;
 KW tobacco; tomato; potato; pepper.
 OS Nicotiana tabacum.
 XX XN W0200299112-A2.
 XX XN 12-DEC-2002.
 XX XN 06-JUN-2002; 2002WO-FR001943.
 XX XN 07-JUN-2001; 2001FR-00007470.
 PR 07-NOV-2001; 2001FR-00014358.
 XX (RHOB-) RHOBIO.
 XX Mene-Saffrane L, Esquerre-Tugaye M, Fournier J, Beffa R;
 PI Grosjean-Cournoyer M;
 XX WPI; 2003-156858/15.
 DR N-PSDB; ABZ68210.
 XX Reducing sensitivity of plants to diseases and pathogens, by
 PT overexpressing a lipoxigenase, also vectors and cassettes for the process
 PT and transformed plants.
 XX Claim 7; Page 39-41; 47pp; French.
 CC The present sequence represents a lipoxigenase-1 (LOX-1) gene. LOX-1 is
 CC an enzyme that catalyses the dioxygenation of polyunsaturated fatty acids
 CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce
 CC the sensitivity of plants to diseases and attack by pathogens.
 CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi
 CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.
 CC tobacco, tomato, potato and pepper
 XX Sequence 862 AA;

QY 195 KYREELNLRGCGTGERKWDRIYDYVDYNDIADDPVGDH--RPILGGTTEYPYPRGR 252
 Db 178 KYREELNLRGCGTGERKWDRIYDYVDYNDIADDPVGDH--RPILGGTTEYPYPRGR 237
 QY 253 TGRPRSRDHYESELSPIMSLDIYVPKDEFGHLMKMSDFLYTLKALISISIKPGLQSI 312
 Db 238 TGRKPTRKDPNSES-----SNDVYLPRDEAFGLKSSDFLYTLGLKSVQNVFLQLQSAF 292
 QY 313 DV--TPNEFDNFKVDNLFERGFPPFNAFKTLTDLTP-PLFKALVRNDGEKLEKPTP 369
 Db 293 DNFTEPRFDSDEVHGYSGIKLPTD----IISKISPLEVLKEIIFRTDGEQALKPFP 348
 QY 370 EVVKNKICWSDEEFAREMLAGNPLIRLEAFPPPTSKLDPNVYGNQNSTITEEHIKH 429
 Db 349 KVIQVSKSAWMTDEEFAREMLAGNPNLRJCKOPPPSKLDSQVYGDHTSQITKEHLEP 408
 QY 430 GLDGLTVDEAMKQNLRIYVDFHDLMPYLTRMNTSTKYATRIALLKDDGTUKPLVIE 489
 Db 409 NLEGLTVDEAIQNKLFLLDHDPIMPYLRRINATSTKAYATRIALLKDDGTUKPLVIE 468
 QY 490 LALPHQDQDLGALISKLYFPAENGCKSIWOLAKAYTVNDVGHOLISHWLHVALEP 549
 Db 469 LSLPHQDQDQSAFQFPLPADEGVESIWLLAKAYVVDNSCHQLVSHWLHVALEP 528
 QY 550 FVIATHROLVSLHPHKLLVPHYKTMFINASARQVLINANGLIETTHYPYSKYSMELSSI 609
 Db 529 FVIATHROLVSLHPHKLLVPHYKTMFINASARQVLINANGLIETTHYPYSKYSMELSSI 588
 QY 610 LYKDWTFDQALPNLMKRGAVESAPHGRLLLINDYPAVDGLDIWSAIAKTMVODYC 669
 Db 589 VYKDWTFDQALPNLMKRGAVESAPHGRLLLINDYPAVDGLDIWSAIAKTMVODYC 648
 QY 670 CLYKDWTFDQALPNLMKRGAVESAPHGRLLLINDYPAVDGLDIWSAIAKTMVODYC 729
 Db 649 FLYKSDDTLREDPELQACWELVEVGHGDKKNEFPWPKMTREELVEACAIITWASAL 708
 QY 730 HAAVNFQGYPGYGLINRPTSRFMPPEKGAEELEARNKPKAYLTKITPKFTLLDLS 789
 Db 709 HAAVNFQGYPGYGLINRPTSRFMPPEKGAEELEARNKPKAYLTKITPKFTLLDLS 768
 QY 790 ITEILSKHASDRVYLQORASIDWTSKIALFAFEKFGKXNLFVEVNERMERKENVLNKRS 849
 Db 769 VIEILSRHASDEVYLGDRNPWTSIDTRALEAFKFGKXNLFVEVNERMERKENVLNKRS 828
 QY 850 GPVNLPTLLVPSSNEGHTGRIPIINSISI 878
 Db 829 GPVNLPTLLVPSSNEGHTGRIPIINSISI 857

RESULT 9
 ID ABG30569 standard; protein; 865 AA.
 AC ABG30569;
 XX 07-OCT-2002 (first entry)
 DT Glycine max low-lipoxygenase 2 (LOX-2).
 DE Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property;
 KW brewing; trans-2-nonenal; flavour stability; storage; shelf-life;
 KW low-lipoxygenase 2.
 XX Glycine max.
 OS WO200253721-A1.
 PN 11-JUL-2002.
 PD 22-JAN-2001; 2001WO-IB000207.
 XX 29-DEC-2000; 2000US-00751687.
 PR 29-DEC-2000; 2000WO-IB002045.

XX (CARL-) CARLSBERG RES LAB.
 PA (HETB-) HEINEKEN TECH SERVICES BV.
 PA (BRAS-) BRASSERIES KRONENBOURG SA.
 XX Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;
 PI Schmitt N, Heister JC, Van Mechelen JR;
 XX WPI; 2002-557742/59.
 DR Novel barley plants having low lipoxygenase activity useful in the
 XX production of plant products such as malt or brewed beverages,
 PT particularly beer having increased stability and flavor.
 PT Disclosure; Fig 22A-B; 112pp; English.
 PS The invention describes a barley plant (I) having a mutant lipoxygenase-1
 XX (LOX-1) protein, the plant or plant portion characterised by a reduction
 CC or absence of LOX activity as compared to a non-mutated control, or
 CC comprising a heterologous nucleic acid sequence expressing an antisense
 CC sequence to a transcribed region of barley lpx-1 gene, operably linked to
 CC a promoter and a transcription terminator sequence. (I), a plant (II)
 CC produced using (I) or a plant product (III) is useful in the manufacture
 CC of a beverage, preferably malt or beer, for stabilising organoleptic
 CC properties of a brewed product over a measured period of time as compared
 CC to a control brewed product produced using a non-mutated barley plant or
 CC its portion, grain or plant progeny, or plant product, and for the
 CC manufacture of a brewed product having reduced levels of free trans-2-
 CC nonenal over a measured period of time or under conditions of elevated
 CC storage temperature, as compared to a control brewed product produced
 CC using a non-mutated barley plant or its portion, grain or plant product.
 CC Beer with significantly enhanced flavour stability is obtained. These
 CC and on exposure to elevated storage temperatures is obtained. These
 CC properties enhance the quality of beer and are useful to extend its shelf
 CC -life and reduce the need to cool beer during transport and storage. This
 CC is the amino acid sequence of the Glycine max low-lipoxygenase 2 (lox-2)
 CC protein
 XX
 SQ Sequence 865 AA;
 Query Match 57.5%; Score 2690; DB 5; Length 865;
 Best Local Similarity 58.4%; Pred. No. 5.4e-235;
 Matches 513; Conservative 127; Mismatches 194; Indels 44; Gaps 8;
 QY 23 VINAGNILDVSSLGKNGKIKGVILMRSNVLDTFEH-----SNLL 64
 Db 10 ILNRG-----GGHKIKGTVMKRNKLVDFNSVADLTGKNGVGLIGTLNVLVSTL 59
 QY 65 DNFTLLGGVGFQLISATHTSNDKRGKNGKAYLERWLTSTIPPLFAGESVFQINFWDE 124
 Db 60 DNLTAFLGESVALQISATKPLANGKGVKDTFLEGIIVSLPTLIGAGESAFNIQFWE 119
 QY 125 NFGFCAPPIKNGHTSEFLKSLTLDVPGVGRVDFDCNSWVPSGRYKRIIPANHY 184
 Db 120 SMGIPGAFIKNYMQVEFLKSLTLEDVFNOCSTIFVCSNWTYNTKYSRIFPANTY 179
 QY 185 LPSQTNPLKRYREBELNLRGDKGERKWDRIYDYVDYNDIADDPVGDH--RPILGGT 242
 Db 180 VSETPAALVGYREBELNLRGDKGERKWDRIYDYVDYNDIADDPVGDH--RPILGGT 239
 QY 243 TYPYPRRGRTGRPRSRDHYESELSPIMSLDIYVPKDEFGHLMKMSDFLYTLKALIS 302
 Db 240 STHPYPRRGRTGRYPTKQDNSEK-----PGEVYVPRDENFGLKSSDFLYGKLSLQ 293
 QY 303 SIKPGLQSIQFV--TPNEFDNFKVDNLFERGFPPFNAFKTLTDLTPLEKALVRNDG 360
 Db 294 YVLPAFESVDFLNFTEPRFDSQDVRDLHEGKILPTVEISTI---MPLPVKELFRD 350
 QY 361 EKFLFPPTPEVVKNDKIKGMSDTEEFAREMLAGNPLIRLEAFPPPTSKLDPNVYGNQNS 420
 Db 351 EQVLKFPFPPIVQVSKSAWMTDEEFAREMLAGNPNLRJCKOPPPSKLDSQVYGDHTSQITKE 410
 QY 421 TITEEHIKGLDGLTVDEAMKQNLRIYVDFHDLMPYLTRMNTSTKYATRIALLKDDGTUKPLVIE 480

411 KITADAL-DLDGYTDEALASRELFLMLDYHDVPMPIRINQTYAKAYATRIPLFREN 468
481 GTLKLVLIELALPHQDQOLGAIKLYPPAENGQVQKSIWOLAKAYVTVNDVGHOLISHW 540
469 GTLKPVAIEUSLPHAGDLSGAVSQVILPAKEGVESTIWLLAKAYVVNDSCYHQLMSHW 528
541 LHTHAVLEPPFVIAITHROLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIETTHYPS 600
529 LNTHAVLEPPFIATNRHLSALHPHYKLLTTHYRDTMNAIARQSLINADGIEKSLFPS 588
601 KYSMELSSILYKDWTFDQALPNNLMKRGGLAVEDSSAPHGLRLILLINDYPFAVDGLDIWSA 660
589 KHSVEMSAVYKNVFTDQALPADLIRGVAIKDPSAPHGLRLIETDYPYAVDGLLEIWA 648
661 IKTWQDYCCLYKDDNAVQNDPELQSWNELREKGHADKHEBWPWKMTLSLIEBCT 720
649 IKTWQEVVSLYIARDDDVDKDESELOQWKEAVEKGHGLDKDKEWPKLOTIEELVEICT 708
721 TIIWIASALHAANFGQYGYGYILNRPPTSSRRPMEVGTABYKELSENPEKAPLRTICS 760
709 IIIWTASALHAANFGQYGYGYILNRPPTSSRRLLPEKGTPEYEMVKSHQKAYLRITIS 768
781 ELQALVSIIEILSKHASDEVYLGORASIDMTSDKIALEAFKFKGNLFEVENRIMERN 840
769 KFTLVLDUSVIEIISRHASDEVYLGORDNPHTWSDSKALQAFQKGNLKEIEKJARKN 828
841 KEVNLKNSRGPVNLYPYLLVPSSNEGLTGRGIPNSISI 878
829 NDQSLNRLGVPQLPYLLHPNS-EGLTGCRGIPNSISI 865

RESULT 10
AAR24042
ID AAR24042 standard; protein; 864 AA.
XX AAR24042;
XX AAR24042;
XX AAR24042;
DT 08-DEC-1992 (first entry)
XX Lipoxigenase.
XX Soybean; transformation; disease resistant; pest resistant.
XX Glycine max.
XX JP04144687-A.
XX 19-MAY-1992.
XX 05-OCT-1990; 90JP-00266687.
XX 05-OCT-1990; 90JP-00266687.
XX (MTS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX WPI; 1992-214124/26.
XX N-PSDB; AAQ25591.
XX Structural gene of soybean lipoxigenase - enables mass prodn. of the
PT lipoxigenase and creates plants with high resistance to disease and
PT pests.
XX
XX
XX Disclosure; Fig 1; 7pp; Japanese.
XX
XX The sequence given is soybean lipoxigenase. This protein is expressed in
CC the sprouting time of soy bean. The DNA encoding this sequence can be
CC ligated into a plasmid and this plasmid used to transform E. coli. Using
CC this transformant, mass production of lipoxigenase is possible. It can
CC also be used to create a plant highly resistant against disease and pest
XX
XX Sequence 864 AA;

Query Match 56.5%; Score 2639.5; DB 2; Length 864;
Best Local Similarity 58.0%; Pred. No. 2,1e-230;
Matches 503; Conservative 125; Mismatches 202; Indels 37; Gaps 7;
QY 39 GNKIKGKVLKMSNVLDFTFHS-----NLDNFTTELLGGGVVS 76
DB 8 GOKIKGTVLMKPNVLDNFNAITSIGKGGVIDTATGILGGVSLVGGVDTATSPFGRNIS 67
QY 77 FOLISATHTSNDGRKGVNKAYLERWLTSIPLPAGESVFOINQFOWDNFPPGPAFFIKN 136
DB 68 MQLISATQDGGSGKGVKEVYLEKHLPTLPLGARQDAFSIFFEWDASFGIPGAFYIKN 127
QY 137 GHTSEFFLKSLLDDVPGYGRVHFPCNSWVPSGYSKDRIFFAHNVLPSPQTPNPKRY 196
DB 128 FMTDFFLVSVKLEIDPNHGTIEFVCSWVNFYSKKNRIFVFVNDTLPSPATPLNLY 187
QY 197 REEELNLRGDCGTGERKEWDRIYDVNDIADPDVGRHPRILGCTTETVYVPRRGTGRP 256
DB 188 RKEEELVLRGDCGTGRKODFRIYDVNDLGNPOGGPRPILGSSSYIPPRVRTGRE 247
QY 257 RSRDRHNTVESRLSPIMSLDIYVPKDNFEGHLMKMSDFLGYTLKALISIKPGLQS-IFD-- 313
DB 248 RRTDTPNSEK-----PGEVYVPRDENFGLKSSDFLYGKMSLSDHVIPLFKSAIFOLR 301
QY 314 VTPNEDNPKFVDNLPFERGFPIPPNAFKTLTDLTP-PLFKALVNDGKELKFTPEVV 372
DB 302 VTSSEFSESDVRSYEGGIKLPTD----ILSQISPLPALKEIFRTDGENVLQFPFPHVA 357
QY 373 KDNKIGWSTDEEFAREMLAGNPPLIRLEAPPTSKLDPNVYQNSQNTIEEHKKGILD 432
DB 358 KVSXSGWMTDEEFAREVIAVGNPNVIRLQEPFPPKSTLDPTLYGDTSTIIEKEQLEINMG 417
QY 433 GLTVDEAMKQNLXYIVDFHDLMPYLTRMNTATST-KTYATRTLLLLKDDGLTKPLVIELA 491
DB 418 GVTVEEALSTQRLFDYQDAFIPYLTRINSIPLTAKAYATRIPLFKDDGLTKPLAIELS 477
QY 492 LPHPOGDOLGALSCLYFPAENGQVQKSIWOLAKAYVTVNDVGYHOLISHMLTHAVLEPFV 551
DB 478 KHPDGDNLGPESIVVLPALEGVDSITWLLAKAHVINDSGVHQLVSHLWNTHAVNEPFA 537
QY 552 IATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMELSSILY 611
DB 538 IATNRHLSVLHPHYKLLVPHYRDTNINGLARQSLINADGIEKSFPGKYSIEMSSVY 597
QY 612 KDWTPDQALPNNLMKRGGLAVEDSSAPHGLRLILLINDYPFAVDGLDIWSAIKTWODYCCL 671
DB 598 KMWVFTDQALPADLVKRGGLAIEDPSAPHGLRLIETDYPYAVDGLIWDKATWVHEYSVL 657
QY 672 YIKDNDNAVQNDPELQSWNELREKGHADKHEBWPWKMTLSLIEBCTTIIWIASALHA 731
DB 658 YIPTDAAVQDDELQAWKKEAVEKGHGLKKEKPMWPKMTTDELQSCSIIVWTASALHA 717
QY 732 AVNFGQYPPGYILNRPPTSSRRPMEVGTABYKELSENPEKAFRTICSELOALYSILII 791
DB 718 AVNFGQYPPGYILNRPPTSSRRPMEVGTABYKELSENPEKAFRTICSELOALYSILII 777
QY 792 EILSKHASDEVYLGORASIDMTSDKIALEAFKFKGNLFEVENRIMERNKEVNLKNSRGP 851
DB 778 EILSKHASDEVYLGORASIDMTSDKIALEAFKFKGNLFEVENRIMERNKEVNLKNSRGP 837
QY 852 VNLPTYLLVPSSNEGLTGRGIPNSISI 878
DB 838 VOLPYTLHRSSEGLTFKGIENSI 864

RESULT 11
AAR50220
ID AAR50220 standard; protein; 853 AA.
XX AAR50220;
XX AAR50220;
XX AAR50220;
DT 08-NOV-1994 (first entry)
XX

DE Soybean lipoxigenase L-4.
 KW Soya; Soybean; lipoxigenase L-4; transgenic plant.
 XX Glycine max.
 OS JP06062864-A.
 FN 08-MAR-1994.
 XX 18-AUG-1992; 92JP-00219480.
 XX 18-AUG-1992; 92JP-00219480.
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 XX WPI; 1994-121126/15.
 DR N-PSDB; AAQ44750.
 XX Soybean lipoxigenase L-4 gene - used in the production of transgenic plants.
 PT Disclosure; Page 6-11; 13pp; Japanese.
 XX The soybean lipoxigenase L-4 gene was isolated from a known soybean genomic DNA clone. The gene is expressed at high levels in the cotyledon, hypocotyl, roots and first leaf. The coding region is made up from 9 exons and codes for a protein having 853 amino acids
 XX Sequence 853 AA;
 SQ
 Query Match 55.4%; Score 2591; DB 2; Length 853;
 Best Local Similarity 57.4%; Pred. No. 5.4e-226;
 Matches 492; Conservative 133; Mismatches 204; Indels 28; Gaps 10;
 QY 39 GNKIKGVILMRSNVLDPTFPHS--NLIDNFTLLGGV-----SFQIISATHTS 86
 DB 8 GQKIGTVMVQKNVLDINSITSVGGIVDQGLGFGISAVDALTPAATKISQILISAT-KA 66
 QY 87 NDSRGKGNKAYLERWLTISPLPAGESVFQINQWENDFGPGAFPIKNGHSEPLKS 146
 DB 67 DGGKGIKGNLNRKGI-TLPTLAGEQAYDWNFDWSDFGIPGAFYIKFMQNEFYLS 125
 QY 147 LTLDVPGYGVHPCNSWVYPSGRYKDRIFPANHVVLPSTNPLRKYREELWNLRG 206
 DB 126 LILEDIPNHGTHIFVCSWVNSKNYKTDRIFFANNYLPSETPAPLLKYREELKNVRG 185
 QY 207 DGTGERKWDRIYDVYVNDIADPDVGH--RPILGTTETYPYPRRGTRGRPRRDHNY 264
 DB 186 DGTGERKWDRIYDVYVNDLGNPDGDKYARPVLGSA-LPYPRRRTGRGTRKDPNS 244
 QY 265 ESRLSPIMSLDIYVPCDNFGLKMSDFGLTKALSIKPGLSIFD--VTPNEPDFNF 322
 DB 245 EK-----PSDFVYLPDRBAFHLKSSDFLAYGKSVQDVLPLVTDADGNILSLEPDFNF 299
 QY 323 KEVDNLFERGFPIPFNAFKLTLEDLTPPLFKALVRNDGERKPLKPTPEVVKDNKNGWSTD 382
 DB 300 AEVHKLYEGGVTLPTN--FLSKIAPIPVKEIFERTDGEQFLKYPPEPKVMQVDSAMWTD 356
 QY 383 BEFARMLAGNPLLIRLEAFPPPTSKLDPNVQNSSTTEHIKHGLDGLTVDEAMKQ 442
 DB 357 BEFARETIAGLNPNVKEIEFFUSKLDLTQAYGDHCTIIAKEHLEPNLGLTVQEAQN 416
 QY 443 NRLYIVDFHDMPLYTERMATSTKTYATRTLLKDDGTLKPLAVIELALPHFGQDLGA 502
 DB 417 KKLFLDHDHLYLPLRKINANTKTATRTIFFLKDDGTLTPLAIELSKPHFQGEYGP 476
 QY 503 ISKLYFPBENGQKSIWOLAKAYTVNDVGHQILSHWLTHAVLEFPVIAHQRLSVLH 562
 DB 477 VSEVYVPASEGVBEAYIMLLAKAYVVDNDACVHQIISHWLSHTAIVEFPVIAHQRLSVH 536
 QY 563 PIHKLVLPHYKDTWTFINASARQVLINAGLTETHTYPSKYSMELSLIYKDWTFPPQALP 622

DB 537 PIYKLLFPHYDTMNSLARKALVADGIIETKFTLWGRYSMEMSAVIYKDWVFTDQALP 596
 QY 623 NNLKRGGLAVEDSSAPHGLRLILNDYPAVGLDITWSAIKTKTWQDYCCLYYKDDNAVQND 682
 DB 597 NDLVTRGVAVKPSAPHGVRLIEDYFASDGLTEWDAIKSWQVYFVSFYKSEELQKD 656
 QY 683 FELQSWNELREKHKHAKHPWPKMTLSBELIESCTTIWIASALHAANFGQYPIYG 742
 DB 657 PELQAWKVELVEVGHGDLKDEWQKQVTRBELVEASAILIWIASALHAANFGQYPIYG 716
 QY 743 YILNRPSTSRFMPVGTAYKELESNEPEKAFIRTCSELQALVSIISIIELSKHASDEV 802
 DB 717 LILNRPSTSRFMPPEKSPYDALAKNPEKFLTKITGKKTLDLTIVIELSRHASDEF 776
 QY 803 YLQQRASID-WTSDKIALEAFKFGKLFVEVNRIMERNKEVNLKRSQVNLPTLLVP 861
 DB 777 YLQQRDGGDYWTSAGPLEAFKFGKLEIEKLEKKNKDETLNRYGPAKMPVTLIYP 836
 QY 862 SSNEGLTRGIPNSISI 878
 DB 837 SSEGLTRGIPNSISI 853
 RESULT 12
 ABG30568
 ID ABG30568 standard; protein; 839 AA.
 XX AC ABG30568;
 XX DT 07-OCT-2002 (first entry)
 XX Glycine max low-lipoxygenase 1 (LOX-1).
 XX Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property; brewing; trans-2-nonenal; flavour stability; storage; shelf-life;
 XX low-lipoxygenase 1.
 XX Glycine max.
 XX WO200253721-A1.
 XX 11-JUL-2002.
 XX 22-JAN-2001; 2001WO-IB000207.
 XX 29-DEC-2000; 2000US-00751687.
 XX 29-DEC-2000; 2000WO-IB002045.
 XX (CARL-) CARLSBERG RES LAB.
 XX (HETB-) HEINEKEN TECH SERVICES BV.
 XX (BRAS-) BRASSERIES KRONENBOURG SA.
 XX Douma AC, Dodderer A, Cameron-Mills V, Skadhauge B, Bech LM;
 XX Schmitt N, Heistek JC, Van Mechelen JR,
 XX WPI; 2002-557742/59.
 XX Novel barley plants having low lipoxygenase activity useful in the production of plant products such as malt or brewed beverages, particularly beer having increased stability and flavor.
 XX Disclosure; Fig 22A-B; 112pp; English.
 XX The invention describes a barley plant (i) having a mutant lipoxygenase-1 (LOX-1) protein, the plant or plant portion characterised by a reduction or absence of LOX activity as compared to a non-mutated control, or comprising a heterologous nucleic acid sequence expressing an antisense sequence to a transcribed region of barley lpx-1 gene, operably linked to a promoter and a transcription terminator sequence. (ii), a plant (iii) produced using (i) or a plant product (iii) is useful in the manufacture of a beverage, preferably malt or beer, for stabilising organoleptic properties of a brewed product over a measured period of time as compared to a control brewed product produced using a non-mutated barley plant or

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2004, 11:56:59 ; Search time 49.1316 Seconds
(without alignments)
922.575 Million cell updates/sec

Title: US-09-937-908-1
Perfect score: 4675
Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVPSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/6CTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2791	59.7	857	4	US-09-751-687-17
2	2690	57.5	865	4	US-09-751-687-16
3	2582.5	55.2	839	4	US-09-751-687-15
4	2524.5	54.0	864	4	US-08-810-268-3
5	2438	52.1	862	4	US-09-751-687-9
6	2431	52.0	862	4	US-09-751-687-12
7	2424	51.9	864	4	US-09-751-687-18
8	495.5	10.6	677	3	US-09-061-768A-4
9	495.5	10.6	677	4	US-09-764-246-4
10	484	10.4	711	4	US-09-547-435-2
11	484	10.4	867	4	US-09-547-435-24
12	479	10.2	556	4	US-09-547-435-6
13	473	10.1	676	3	US-09-061-768A-2
14	473	10.1	676	4	US-09-764-246-2
15	466	10.0	692	4	US-09-252-991A-19668
16	457.5	9.8	701	3	US-09-087-727-2
17	457.5	9.8	701	4	US-09-853-053-2
18	427.5	9.1	662	3	US-09-061-768A-25
19	427.5	9.1	662	4	US-09-764-246-25
20	426.5	9.1	663	4	US-09-641-638-653
21	416.5	8.9	582	3	US-09-413-814-83
22	409.5	8.8	615	4	US-09-547-435-10
23	409.5	8.8	771	4	US-09-547-435-28
24	404.5	8.7	460	4	US-09-547-435-12
25	359	7.7	291	4	US-09-547-435-14
26	284.5	6.1	195	4	US-09-547-435-20
27	238	5.1	489	4	US-09-547-435-4

28	238	5.1	645	4	US-09-547-435-26	Sequence 26, Appl
29	233	5.0	334	4	US-09-547-435-8	Sequence 8, Appl
30	137	2.9	925	4	US-09-924-097A-14	Sequence 14, Appl
31	135.5	2.9	1541	3	US-08-296-791-3	Sequence 3, Appl
32	135.5	2.9	1541	4	US-09-839-996-3	Sequence 3, Appl
33	135.5	2.9	1541	4	US-10-080-505-3	Sequence 3, Appl
34	135.5	2.9	1541	5	PCT-US95-10661A-3	Sequence 3, Appl
35	134.5	2.9	139	4	US-09-547-435-18	Sequence 18, Appl
36	126.5	2.7	990	2	US-08-392-625-20	Sequence 20, Appl
37	126.5	2.7	990	2	US-08-466-961A-20	Sequence 20, Appl
38	120	2.6	990	2	US-08-645-193B-15	Sequence 15, Appl
39	113.5	2.4	945	4	US-09-198-452A-1030	Sequence 1030, Ap
40	113	2.4	69	4	US-09-547-435-16	Sequence 16, Appl
41	110.5	2.4	720	2	US-08-840-238-1	Sequence 1, Appl
42	110.5	2.4	720	2	US-08-505-448A-1	Sequence 1, Appl
43	110	2.4	514	4	US-09-540-236-2267	Sequence 2267, Ap
44	109.5	2.3	1545	3	US-08-296-791-4	Sequence 4, Appl
45	109.5	2.3	1545	4	US-09-839-996-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-751-687-17
; Sequence 17, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Rech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-17

Query Match	59.7%;	Score 2791;	DB 4;	Length 857;
Best Local Similarity	60.3%;	Pred. No. 9.3e-267;		
Matches 524;	Conservative 131;	Mismatches 182;	Indels 32;	Gaps 7;
Qy	28	GMLDRVSSLGNGKIKGVILMRNVLDFTPEHS	-----NLLDNFTLLGGG	74
Db	3	GGLLHR-----GHKIKGTIVLMRKNVLDVNSVTSGGIQGLDLVGLSTLDTLTAFLGRS	57	
Qy	75	VSFQILSATHTSNDGRGKVGKXAYLERWLTSTIPPLPAGESVFQINFQNDENFGFGAPPI	134	
Db	58	VSLQLISATKADANGKGLKATFLEGIITSITLTCAGQSFKINFEWDGSGIFQAFVI	117	
Qy	135	KNGHTSEFFKSLTLDDVEGYGRVHFDGNSWYPSGRYKDRIFPFANHYVLPSTPNPLR	194	
Db	118	KNFQTEFFLVSLTLEDIENHGSIFHCNSWYNAKLPKSDRIFFANQYLPSTPAPLV	177	
Qy	195	KYREELNLRGDDGGERKEWDRIYDYVYNDIADPDYGDH--RPLGGTTEYPPYPRGR	252	
Db	178	KYREELNLRGDDGGERKEWRIYDYVYNDIADPDYGDH--RPLGGTTEYPPYPRGR	237	
Qy	253	TGRPSRRDHNYESRLSPIMSLDIYVPKDNFENHGLKMSDFLGYTLKALISIKPGIQTIF	312	
Db	238	TGRKPTRKDPNSES-----SNDVYLPRDEAFGLKSSDFLYGLKSVQNVLPQLQSAF	292	
Qy	313	DV--ITNEFDNKEVDNLFERGFPPFNAFKTLTDLTLP-PLFKALVRNDGKFLKFPPT	369	
Db	293	DLNFTPREDFSDVEHGLYSGGIGKLPD-----IISKISLPVLKIFRDTGDAQLKFPPT	348	

Db 295 DSFDIINLYEGGKLPKVALEELRQKQPLQIKDLPLVGGDSLLKLPVPHIIQENKQA 354
Qy 379 WSTDEEFAREMAGNPLIRLEAFAPPTSKLDENVYGNONSTITEEHIKHGLDGLTVDE 438
Db 355 WRTDEEFAREVLAVNPNWIRLEFPKPSLDSKFGDHTSTITASHIEKNLEGLTVQ 414
Qy 439 AMQNRLYIVDFHDMALPYLTRM-NATSTKTYATRTLLKDDGTLKPLVIELALPHPOG 497
Db 415 ALESNRLYILDHDRFEMFLDVNPLPGNFYATRTLLFLRGDGRLEPLAIELESEPIQG 474
Qy 498 DQLGAKSLKYPFAENG-VOKSIWOLAKAYVTVNDVGVHQLISHWLHVALEPPIATHR 556
Db 475 GLTTAKSKYVTPVSGSVEGWELAKAYAVNDVGVHQLVSHHNLTHAVNEPPIVSTNR 534
Qy 557 QLSVLHPIHKLVLPHYKDTMFINASARQVLINANGLIETTHYPYSKYSMELSSILYKDWTF 616
Db 535 HLSVTHPVHKLSPHYRDTMTNALARQTLINAGGIFEMTFPGKFAIGMSAVVYKDWKF 594
Qy 617 PQALPNMLKRGVAVEDSSAPHLRLILINDYPAVGLDIWSAIKTWVODYCCLYKDD 676
Db 595 TEQGLPDDLIRGMVAVEDSSAPHLRLILINDYPAVGLDIWSAIKTWVODYCCLYKDD 654
Qy 677 NAVQNDPELOSWNELREKKGHADKHEPWPMPKMTLSLBSCTTIIWIASALHAAVNF 736
Db 655 GVLQDTEVQAWKRETEVEGHGDLKDAWPFKMSQVPELAKACTIIWIGSALHAAVNF 714
Qy 737 QYPCGYILNRPPTSRFRMPVEVGTAEYKELESNEPEKAFRTICSELOALVSIISIELSK 796
Db 715 QYVAGFLPNRPPTSRFRMPVEVGTAEYKELESNEPEKAFRTICSELOALVSIISIELSK 774
Qy 797 HASDEVYLGORASIDWTSKIALAEKFKGNLFEVENRIMERNEKVNLRSGPVNLPY 856
Db 775 HSSDELVLQDTEWTSDDKALEVFKFSPDRIVEISKVGVGMNDPELKNRNGPAKFPY 834
Qy 857 TLLVPSSNE-----EGLTGRGIPNSISI 878
Db 835 MLLYVNTSDHKGAAAGLTAKGIPNSISI 862

RESULT 7

US-09-751-687-18
; Sequence 18, Application US/09751687
; Patent No. 6660915

; GENERAL INFORMATION:

; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhaug, Birgitte
; APPLICANT: Bech, Lene

; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY

; FILE REFERENCE: 11225.11US01

; CURRENT APPLICATION NUMBER: US/09/751.687

; CURRENT FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 18

; LENGTH: 864

; TYPE: PRT

; ORGANISM: Hordeum vulgare

US-09-751-687-18

Query Match

Best Local Similarity 51.9%; Score 2424; DB 4; Length 864;

Matches 470; Conservative 143; Mismatches 237; Indels 20; Gaps 9;

Qy 23 VINAGNTLDVRSSIGGNKIKGVILMESNVLDTEPHSNLLDNFTLGGGVSFOLISA 82
Db 1 MLGVGGIVSDLTGGIRGAHLKGSVVLKRNALDNDFGAHVMDGVTELLGRGVTCQLISS 60
Qy 83 THT--SNDSRGKGVGNKAYLERWL--TSIPPLFAGESVQINFOWD-ENFGFPFGAFFIKNG 137
Db 61 TNVDHNNNGRGKVGAEANLEQWLLPTNLPFITTGKFNFAVTFDWSVKLGVPGLIYKNN 120

Qy 138 HTSEFFLKSLTDDVPYGRVHFDNCNSWYPSGRYKDKRIFPANHVLPSQTPNPLRYR 197
Db 121 HASEFFLKSLTDDVPYGRVHFDNCNSWYPSGRYKDKRIFPANHVLPSQTPNPLRYR 180
Qy 198 EELNWLKRGD-TGRKEWDRIVDYVNDIADPDVGDHRPILGCTTEYPYRGRGTGP 256
Db 181 DDELRLNRDQDQGPYLDHVRVYDYVNDL-----GDSRDVLGSKOLPYPRRCRTGRK 235
Qy 257 RRRRDHNVSRSPMSLDIYVYKDNENFGHLKMSDFLGYTLKALISIKPGQSIFDVTP 316
Db 236 PSDSKPDHESRL-LLVQNVYVLRDELFGHLKQSDLLGYTLKGLWDGILAIRTYVDLSP 294
Qy 317 NFPDNFKEVDNLFERGFPI-PNAFKTLEDITLTPFLFALVRNDGEKFLKFTPEVVDN 375
Db 295 GEFDSFADILKLYEGIKLPNIPALEEVRKRPFLQVLDLIPKGGDFLKLKPK8I1KVD 354
Qy 376 KIGWSTDEEFAREMAGNPLIRLEAFAPPTSKLDENVYGNONSTITEEHIKHGLDGLT 435
Db 355 QKAWMTDEEFAREMAGNPNPMIKLTETFPKASTLDPKYGDTMTTEEHVAKSLEGLT 414
Qy 436 VDEAMQNRLYIVDFHDMALPYLTRM-NATSTKTYATRTLLKDDGTLKPLVIELALPH 494
Db 415 VQALAGNELYIVDQHDNLMPELIDINLDASFVYATRTLLFLRGDGTLPVAILSSPL 474
Qy 495 PGDDQLGAKSLKYPFAENG-VOKSIWOLAKAYVTVNDVGVHQLISHWLHVALEPPIAT 554
Db 475 IQELTAKSAYVTPHAGVEGWELAKAYAVNDVGVHQLVSHHNLTHAVNEPPIAT 534
Qy 555 HQQLSVLHPIHKLVLPHYKDTMFINASARQVLINANGLIETTHYPYSKYSMELSSILYKDW 614
Db 535 NQLSVTHPVHKLSPHYRDTMTNALARQTLINAGGIFEMTFPGKFAIGMSAVVYKDW 594
Qy 615 TFPDQALPNMLKRGVAVEDSSAPHLRLILINDYPAVGLDIWSAIKTWVODYCCLYK 674
Db 595 NFTEQALPADLIRGMVAVEDSSAPHLRLILINDYPAVGLDIWSAIKTWVODYCCLYK 654
Qy 675 DDNAVONDELOSWNELREKKGHADKHEPWPMPKMTLSLBSCTTIIWIASALHAAV 734
Db 655 NCGVLQDTEVQAWKRETEVEGHGDLKDAWPFKMSQVPELAKACTIIWIGSALHAAV 714
Qy 735 FGQYVGGYILNRPPTSRFRMPVEVGTAEYKELESNEPEKAFRTICSELOALVSIISIEL 794
Db 715 FGQYVGGYILNRPPTSRFRMPVEVGTAEYKELESNEPEKAFRTICSELOALVSIISIEL 774
Qy 795 SKHASDEVYLGORASIDWTSKIALAEKFKGNLFEVENRIMERNEKVNLRSGPVNLPY 854
Db 775 SKHSDEVYLGQDTEWTSDDKALEVFKFSPDRIVEISKVGVGMNDPELKNRNGPAKFP 834
Qy 855 PYTLVPSSNE-----EGLTGRGIPNSISI 878
Db 835 PYMLYVNTSDHKGAAAGLTAKGIPNSISI 864

RESULT 8

US-09-061-768A-4

; Sequence 4, Application US/09061768A

; Patent No. 6204037

; GENERAL INFORMATION:

; APPLICANT: BRASH, ALAN R.

; APPLICANT: BOEGLIN, WILLIAM E.

; APPLICANT: JISAKA, MITSUO

; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

; CITY: DURHAM CAROLINA

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

; COMPUTER: IBM PC/XT/AT compatible

Db 208 -----WRSUREMRLP-----NFRKTPA 225
QY 369 PEVVKDNKIGNSTDEFAREMLAGNPLLIIRLEAPP-----TSKLDPNVYGNQNSTITE 424
Db 226 ASYVFAH---WQEDAFASQFLNGINPVLIERCHSLP-----NNFPVTDWVA 270
QY 429 HGL-DGLTVDEAMQNRLIYVDFHDLMPYLTR-MNATSTKYATRTLL-LLKDDGTILKP 485
Db 271 FVLGPGTSLQAELEKSGSLFDV-HGILSGVHTNLNGKPOFSAAPMTLLHQSSGSGPLLP 329
QY 486 LVIEL-ALPHPGQDQLGAISKLYPPAENGQVKS-WOLAKAVTVTVNDVGVHQLISHMLH 544
Db 330 IAIQLKQTPGPD-----NPIFLPSDDTDW---WLLAKTVWNSSEFYIHEAVTHLLAH 379
QY 545 AVLPEFVIAHQRLSVLPHIHLVPHYKOTMFINASARQVLINANGLI-ETHYPSKY 603
Db 380 LIPEVFALATLRLQPRCHPLFKLLPHIRYTLHINTLARELLVAPGKLIDKSTGLGTGGF 439
QY 604 MELASILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGLRLINDYPFAVDGLDIWSA 662
Db 440 SLLIKRNEQUNYSVLCPEDIRARG--VED-----IPGYTRDDGMQIWAIGAKS 487
QY 664 WVQDYCYLYKDDNAVQNDFFELQSWNNELEKKGHADKKHEPFWPMQOTLSLIESCTTII 723
Db 488 FVSEIVSYIYPSDTSVQDDQLQAWREIFPSEGFLGREGSGMPSSLDTREALVQYITMVI 547
QY 724 WIASALHAANVFGQYVGGYILNRPPTTSRRPMPVGTAEYKESNEPEKAFLEKTCISELQ 783
Db 548 FTCSAKHAASVSGQFDCVWMPNLPTMQLPPT-----SKQARPE-SFIATLPAVNS 600
QY 784 ALVSIISIILSKHASDEVILGORASIDWTS--KIALEAFKFGKNLFEVENRIMERNK 841
Db 601 SSYHIIALWLSABPGDQRLGHVDFEHTEDAPRSVAAFQ---RKLIQISKIGIRENR 657
QY 842 EVNLKRGSPVNLPTLLVPSSNEGLTGRGIPNSISI 878
Db 658 -----GLALPYTYLDPL-----IENSVSI 677

RESULT 10
US-09-547-435-2
; Sequence 2, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-2

Query Match 10.4%; Score 484; DB 4; Length 711;
Best Local Similarity 25.5%; Pred. No. 2e-38;
Matches 163; Conservative 114; Mismatches 217; Indels 146; Gaps 21;
QY 306 PGLQSFIDVTPNEFDNFKVED-----NLFERGFP----- 334
Db 151 PGFPCMVDPV-----NSFQEMESDKKFKALTCTTCVDQDSSGNRYLPGFPMKIDIPSLMY 205
QY 335 -----IPFNAFKLTLEDLTPPLFKALVRNDGEKFL-----KFFT 368
Db 206 MEPNVRYSATKTIIS-----LLFNAIPASLGMKRLGLLDRKSGWKLLDDMQNIFWCHKTFT 260

QY 369 PEVVKDNKIGNSTDEFAREMLAGNPLLIIRLEAPP-----TSKLDPNVYGNQNSTITE 424
Db 261 TKYVTEH---WCEDHFFGVQYLVGNVPVMLHCISLPSKLPVNDWAPLLQDTCLOTE 317
QY 425 EHIKGLDGLTVDEAMQNRLIYVDFHDLMPYLTMNATSTKYATRTLLIIXDDGTILK 484
Db 318 -----LERGNIFLADYWIILAEAPTHCLNGRQOYVAAPLCLLWLSQGALV 362
QY 485 PLVIEIA-LPHPGQDQLGAISKLYPPAENGQVKS-IWQAKAVTVTVNDVGVHQLISHMLHT 543
Db 363 PLAIQLSQTGPD-----SPIFLPTDS---EWDMLLAKTVWNSSEFLVHENNTFLCT 412
QY 544 HAVLPEFVIAHQRLSVLPHIHLVPHYKOTMFINASARQVLINANGLI-ETHYPSKY 602
Db 413 HLLCEAFAMATLRLQPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVQDVTSIGRQG 472
QY 603 SMELASILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGLRLINDYPFAVDGLDIWSA 662
Db 473 LYLIMSTGLAHFTYINFLCPDSLRGV-----LAI PNHYRDDGLKIWAILE 520
QY 663 TWQDYCYLYKDDNAVQNDFFELQSWNNELEKKGHADKKHEPFWPMQOTLSLIESCTTII 722
Db 521 SFVSEIVGYIYPSDTSVQDDSELQAWTGEIFAQAFLGREGSGFPRLCTPGEMVFLTAI 580
QY 723 IWTASALHAANVFGQYVGGYILNRPPTTSRRPMPVGTAEYKE-LESNEPEKAFLEKTCIS 780
Db 581 IFNCSAQHAANVSGQHDGFMWPNAPSSWRQPPQTKGTTILKTYLDLPE---VNISCN 637
QY 781 ELQALVSIISIILSKHASDEVILGORASIDWTS--KIALEAFKFGKNLFEVENRIME 838
Db 638 NL-----LLFVLVSGQPKDQRLPTGTYPDHFTEDAPRSVAAFQ---SRLAQISRDIOE 688
QY 839 RKEVNLKRGSPVNLPTLLVPSSNEGLTGRGIPNSISI 878
Db 689 RNQ-----GLALPYTYLDPL-----IENSVSI 711

RESULT 11
US-09-547-435-24
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-24

Query Match 10.4%; Score 484; DB 4; Length 867;
Best Local Similarity 25.5%; Pred. No. 2.8e-38;
Matches 163; Conservative 114; Mismatches 217; Indels 146; Gaps 21;
QY 306 PGLQSFIDVTPNEFDNFKVED-----NLFERGFP----- 334
Db 307 PGFPCMVDPV-----NSFQEMESDKKFKALTCTTCVDQDSSGNRYLPGFPMKIDIPSLMY 361
QY 335 -----IPFNAFKLTLEDLTPPLFKALVRNDGEKFL-----KFFT 368
Db 362 MEPNVRYSATKTIIS-----LLFNAIPASLGMKRLGLLDRKSGWKLLDDMQNIFWCHKTFT 416


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QY 682 DPELQSWNNELREKGHAKDKHEPWPWKMTLSLIESCTTIWIASGALHAANVFGQYPYG 741A
Db 505 DRELQAWREIEIFSKGLNQSSGIPSSILETREALVQVVTWVIFTCSAKHAASAGQDFSC 564
QY 742 GYLINRPTTSRRFMPE--VGTAEYKELESNPEKAPLRTI-----CSELQALVSTSIIE 792
Db 565 AWPVNLPSMQLPPTTSKGLATC-----GFIATLPFVNATCDVILAL-----W 608
QY 793 ILSKASDEVILYQORASIDWTSDKIALAEAFKFGKNLFEVENRIMBERKEVNLKNRSGEV 852
Db 609 ILSKSPGDRPLGTPDSEHFT--EEAPRRSIATFQSLAQISRGIQERNR-----GLV 659
QY 853 NLPYTLILYPSSNEGTLGRGIPNSISI 878
Db 660 -LPYTLDPPL-----IENSVSI 676

RESULT 15
US-09-252-991A-19668
; Sequence 19668, Application US/09252991A
; Patent NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDO
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19668
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19668

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596 EADLKKMPPTVALEKKNYHLLG----SVHGRLGDRQTFYPAPVFSDDRRVTASG 650
      | : | : | | | : | | | : | | : | | : | | : | | : |
822 --FEFGKGLPEVENRIMERKENVKNRGPVNLPYTLVPSNBSGLTCRGTPNSISI 878
      | : | : | | | : | | | : | | | : | | | : | | : |
651 GLEPFOARLKEVATINRQ-----PVEYLLPSR-----IPASTNI 692
      | : | : | | | : | | | : | | | : | | | : | | : |

```

Search completed: July 16, 2004, 12:05:02
Job time : 53.1316 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2004, 11:33:03 ; Search time 25.4756 Seconds
(without alignments)
1794.561 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675

Sequence: 1 MFGIGKNIIEGALTGTGLA.....LVFSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2955	63.2	860	1 LOXA LYCES	P38415 lycopersico
2	2932	62.7	861	1 LOX1 SOLTU	P37831 solanum tub
3	2847	60.9	859	1 LOX1 ARATH	Q06327 arabidopsis
4	2812.5	60.2	859	1 LOXB LYCES	P38416 lycopersico
5	2769	59.2	857	1 LOX3 SOYEN	P09186 glycine max
6	2705.5	57.9	864	1 LOX2 PEA	P09918 pisum sativ
7	2696.5	57.7	861	1 LOX3 PEA	P09439 glycine max
8	2690	57.5	865	1 LOX2 SOYEN	P24095 glycine max
9	2644.5	56.6	864	1 LOXB PHAVU	P27480 phaseolus v
10	2596	55.5	862	1 LOXA PHAVU	P27480 phaseolus v
11	2591	55.4	853	1 LOX4 SOYEN	P38417 glycine max
12	2582.5	55.2	839	1 LOX1 SOYEN	P08170 glycine max
13	2546	54.5	866	1 LOX1 LENCU	P38414 lens culina
14	2438	52.1	862	1 LOX1 HORVU	P29114 hordeum vul
15	2415	51.7	741	1 LOXB PHAVU	P27481 phaseolus v
16	2390.5	51.1	865	1 LOX2 ORYZA	P29250 oryza sativ
17	1740	37.2	896	1 LOXC ARATH	P38418 arabidopsis
18	1665	35.6	896	1 LX23 HORVU	Q89sm2 hordeum vul
19	1656	35.4	923	1 LOXC ORYZA	P38419 oryza sativ
20	1532.5	32.8	936	1 LX21 HORVU	P39184 hordeum vul
21	1508	32.3	932	1 LX22 HORVU	Q89sm3 hordeum vul
22	569	12.2	1066	1 AOSL PLEHO	O16025 pleura ho
23	516.5	11.0	673	1 LOX5 HUMAN	P09917 homo sapien
24	515.5	11.0	673	1 LOX5 MOUSE	P48999 mus musculu
25	510	10.9	672	1 LOX5 MESAU	P51399 mesocricetu
26	500	10.7	662	1 LOXE MOUSE	P55249 mus musculu
27	498.5	10.7	711	1 LXB3 MOUSE	Q9wv07 mus musculu
28	495.5	10.6	677	1 LX1B MOUSE	O35936 mus musculu
29	495	10.6	672	1 LOX5 RAT	P12527 rattus norv
30	484	10.4	711	1 LXB3 HUMAN	Q9byj1 homo sapien
31	473	10.1	676	1 LX1B HUMAN	O15296 homo sapien
32	469	10.0	662	1 LOXP RABIT	O15043 oryctolagus
33	466	10.0	662	1 LOXL1 MOUSE	P39654 mus musculu

RESULT 1
LOXA LYCES
ID LOXA LYCES STANDARD; PRT; 860 AA.
AC P38415;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxigenase A (EC 1.13.11.12).
GN LOX1.1 OR LOXA.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Caruso; TISSUE=Pericarp;
RX MEDLINE=95062736; PubMed=7972514;
RA Ferrie B.J., Beaudoin N., Burkhardt W., Bowsher C.G., Rothstein S.J.;
RT "The cloning of two tomato lipoxigenase genes and their differential
expression during fruit ripening.";
RL Plant Physiol. 106:109-118(1994).
CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
hydroperoxyoctadeca-9,11-dienoate.
CC -1- COFACTOR: Iron, one atom tightly bound per molecule.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN GERMINATING SEEDS AS WELL AS IN
RIPENING FRUIT.
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.

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CC EMBL; U09026; AAA53184.1; -;
DR HSPSP; P08170; 2SBL.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.

ALIGNMENTS

P13530 oryctolagus
O70582 mus musculu
O75342 homo sapien
P16469 sus scrofa
P27479 bos taurus
P18054 homo sapien
P39655 mus musculu
Q02759 rattus norv
P16050 homo sapien
P42782 haemophilus
P56785 arabidopsis
P30195 staphylococ

34 463.5 9.9 662 1 LOX1 RABIT
35 459 9.8 701 1 LOXR MOUSE
36 457.5 9.8 701 1 LOXR HUMAN
37 453 9.7 662 1 LOXP FIG
38 443 9.5 662 1 LOXP BOVIN
39 441.5 9.4 662 1 LOXP HUMAN
40 435 9.3 662 1 LOXP MOUSE
41 433 9.3 662 1 LOX2 RAT
42 427.5 9.1 661 1 LOX1 HUMAN
43 135.5 2.9 1541 1 IGAL HAEIN
44 125 2.7 1786 1 YCF1 ARATH
45 119 2.5 986 1 EPIB STAEP

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DR PROSITE; PS0095; PLAT; 1.  
KW Oxidoreductase; Dioxxygenase; Iron; Multigene family.  
FT DOMAIN 29 159  
FT METAL 521 521 IRON (BY SIMILARITY).  
FT METAL 526 526 IRON (BY SIMILARITY).  
FT METAL 712 712 IRON (BY SIMILARITY).  
FT METAL 860 860 IRON (BY SIMILARITY).  
SQ SEQUENCE 860 AA; 96764 MW; 43D1091853469426 CRC64;  
  
Query Match  
Best Local Similarity 63.2%; Score 2955; DB 1; Length 860;  
Matches 548; Conservative 129; Mismatches 176; Indels 14; Gaps 5;  
  
QY 17 GDLASVINAGNIIDRVSSLGKNIKGVILMRNVLDTFFHNSLNDNTFELLGGVVS 76  
DB 3 GOLVGLI--GGH-----HDSKVKVGTVMVMKKNALDFTDLAGSLTKDFEALGQKVS 53  
  
QY 77 FOLISATHT--SNDGRGKGVNKAYLERMLTSPPLFAGESVFOINFDNDNFGFGPAFFI 134  
DB 54 FOLISVQSDPANGLOQKHSNPALENFLLTLTPLAGETAFGVTFDWNNEFGVPGAFVI 113  
  
QY 135 KNGHTSEFLKSLTLDVPGYGRVHFCNSWYPSGRYKDRIFPANHVLPSQTPNPLR 194  
DB 114 KMHINEFLKSLTLEDVNHGVHFCNSWYPSGRYKDRIFPANHVLPSQTPNPLR 173  
  
QY 195 KYREELNLRGDTGERKEWDRIYDYVNDIADPVDGH--RPILGGITYEYPRGR 252  
DB 174 KYREELNLRGDTGERKEWDRIYDYVNDIADPVDGH--RPILGGITYEYPRGR 233  
  
QY 253 TGRPSRDRHYESRLSPMSLDIYVPDENFGHLKMSDFGLYTKALSIKPGLOSIF 312  
DB 234 TGRPRTDPKSESRIPLISLDIYVPRDERFHLKMSDFGLYTKALSIKPGLOSIF 293  
  
QY 313 DVTNEFNKVDNLPFRGPPIPN--APKILTEDLTPPLFKALVRNDGEKLFKFPPEV 371  
DB 294 DGTNPFSDFDVLYLVEGGIKLPGPLFKALTDAPLEMIRELLRTDGEILFPFPLV 353  
  
QY 372 VNDKIGWSTDEFAREMLAGNPLIRLEAFPTSKLDPNVYGNONSTTTEHIXHGL 431  
DB 354 IKDSKATRTDEFAREMLAGNPNVILSELEFPFKSLDDELNGONSTTTEHIXHGL 413  
  
QY 432 DGLTVDEANKQNLVIVDFHDMPLTRMNASTKTVATLTLLKDDGTLKPLVIELA 491  
DB 414 DGLTIDEAINSKPLFLNHHDVLPYLRINTTTTKTVASRTLLFLODNGSLKPLATELS 473  
  
QY 492 LPHPGDGLGATSKLYFPAENGVOKS IWLAKAYVTVNDVGYHOLISHWLTHAVLEPFV 551  
DB 474 LPHPGDGLGATSKLYFPAENGVOKS IWLAKAYVTVNDVGYHOLISHWLTHAVLEPFV 533  
  
QY 552 IATHQSLVLPHPHKLPHYKDTMFINASARQVLINANGLIETHYPSKYSMLLSILY 611  
DB 534 IATHQSLVLPHPHKLPHYKDTMFINASARQVLINANGLIETHYPSKYSMLLSILY 593  
  
QY 612 KDWTPDQALPNLMKRGSLAVDSAPHLRLINDYPAVDGLDIHSAIKTVQDYCCCL 671  
DB 594 KDWTPDQALPNLMKRGSLAVDSAPHLRLINDYPAVDGLDIHSAIKTVQDYCCCL 653  
  
QY 672 YKQDNVQNDVQLQSWNLEKREKADKKEHPWPKMOTLSIELSCITTIWIASALHA 731  
DB 654 YKQDNVQNDVQLQSWNLEKREKADKKEHPWPKMOTLSIELSCITTIWIASALHA 713  
  
QY 732 AVNFQCYGYGILNRPRTTSRFRPEVGTABYKLESNPEKAFRTICSELOALVSIISII 791  
DB 714 AVNFQCYGYGILNRPRTTSRFRPEVGTABYKLESNPEKAFRTICSELOALVSIISII 773  
  
QY 792 BILSHASDEVYLGORASIDWTSKIALEAPKFKGNLFEVENRIMERNEKVNILKRSQP 851  
DB 774 BILSHASDEVYLGORASIDWTSKIALEAPKFKGNLFEVENRIMERNEKVNILKRSQP 833  
  
QY 852 VNLPTLLVPSNEGLTGRGIPNSISII 878  
DB 834 VNLPTLLVPSNEGLTGRGIPNSISII 860
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RESULT 2  
LOX1 SOLTU STANDARD; PRT; 861 AA.  
ID LOX1 SOLTU  
AC P37831; 1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Lipoxxygenase 1 (EC 1.13.11.12).  
GN LOX1.1 OR LOX1.  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Desiree; TISSUE=Tuber;  
RX MEDLINE=95175602; PubMed=7870815;  
RA Casey R.;  
RT "Sequence of a cDNA clone encoding a potato (Solanum tuberosum) tuber  
lipoxxygenase.";  
RL Plant Physiol. 107:265-266(1995).  
CC -I- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO  
WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
CC -I- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
hydroperoxyoctadeca-9,11-dienoate.  
CC -I- COFACTOR: Iron, one atom tightly bound per molecule.  
CC -I- SUBUNIT: Monomer (By similarity).  
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -I- SIMILARITY: Belongs to the lipoxxygenase family.  
CC -I- SIMILARITY: Contains 1 PLAT domain.  
  
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EMBL; X79107; CAA55724.1; -.  
PIR; S44940; S44940.  
HSSP; P09186; LNH.  
InterPro; IPR000907; Lipoxxygenase.  
InterPro; IPR001024; Lipoxxygenase_LH2.  
InterPro; IPR008976; PLAT LH2.  
Pfam; PF00305; lipoxxygenase; 1.  
Pfam; PF01477; PLAT; 1.  
PRINTS; PR00087; LIPOXYGENASE.  
SMART; SM00308; LH2; 1.  
PROSITE; PS00711; LIPOXYGENASE_1; 1.  
PROSITE; PS00081; LIPOXYGENASE_2; 1.  
PROSITE; PS00095; PLAT; 1.  
KW Oxidoreductase; Dioxxygenase; Iron; Multigene family.  
FT DOMAIN 29 160  
FT METAL 522 522 IRON (BY SIMILARITY).  
FT METAL 527 527 IRON (BY SIMILARITY).  
FT METAL 713 713 IRON (BY SIMILARITY).  
FT METAL 861 861 IRON (BY SIMILARITY).  
SQ SEQUENCE 861 AA; 96966 MW; 09732A6751DEE20D CRC64;  
  
Query Match  
Best Local Similarity 62.7%; Score 2932; DB 1; Length 861;  
Matches 543; Conservative 124; Mismatches 174; Indels 10; Gaps 5;  
  
QY 38 GGN-----KIKGVILMRNVLDTFFHNSLNDNTFELLGGVVSFOLISATH--TSNDSRG 91  
DB 11 GGHDDSKVKVGTVMVMKKNVLDFTDLAGSLTGKIFDLVGQKVSFQLISSVQDFTNGLIQ 70
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QY	92	KVGNKAYLERMUTSIPPLFAG-ESVFQINFOWDENFGPCAFIKXGHTSEFPFKSLTLD	150
Db	71	KESNPAYLJENSLLTTPITAGSETAFGVTFDWNESEFGVGAFTIKXGHTSEFPFKSLTLE	130
QY	151	DVPGVGRVHFDGNSWVPSGKYKDRIFFAHNVLPSPOTENLRKYREBELMNLRGDGTG	210
Db	131	DVPNGHKVHFCVNSWVPSLNYKSDRIFFAHNVLPSETPELRLKYRENELLTLRGDGTG	190
QY	211	ERKEWDRYDYVDYNDIADPDVGH-APILGGTTEYPYPRGRGTGRPSRRDHNYESRL	268
Db	191	KREAWDRYDYDYNDLGNPDQCKENVRITLGGSAEYYPYPRGRGTGRPTRTDPKSESRI	250
QY	269	SPIMSDIIVPKDENFGHLKXWSDPLGYTLXKALSISIKPGLQSFDTVTNEFDNFKEVDNL	328
Db	251	PHILSDIIVPKDERFGLKXWSDPLGYTLXKALSISIKPGLQSFDTVTNEFDNFKEVDNL	310
QY	329	FERGFPPIFPN-AFKTLTBDLTPPLFKALVRNDGKFLKFPPTPEYVKNKIGNSTDEEPAR	387
Db	311	YEGGKLPQGPLFKALTAALPLEMIRELLRTDGGILRFPPTPLVTKDSKTAWRTDEEPAR	370
QY	388	EMLAGENPLLIIRIEAPPTSKLDPNVYGNQNSITTEHIIKHGLDGLTVDENAKQNRLYI	447
Db	371	EMLAGVNPVITSLRGEFPFKSLDPEAYGNQNSITTAHIEDKLDGLTVDENAKQNRLYI	430
QY	448	VDFPHALMPLTRMNATKTKYATRTLLLLKXDDGTLKPLVIELALPHPOGDQLGALSKLY	507
Db	431	LNHHDVILPYLRREINTITKAYASKTLLFLQDNGSLAPLALSLSPHPDGDQFGVTSKY	490
QY	508	FPAENGQVKSIIWOLAKAVTVNDVGVYHOLISHWLHTHAVLEPPVIATHROLSVLHPHKL	567
Db	491	TPSDQGVESSIIWOLAKAVAVNDVGVHOLISHWLHTHAVIEPVIATNROLSVLHPHKL	550
QY	568	LVPHYKDTWFINASARQVLINANGLIETHYPSKYSMELSSILYKDWTPPDQALPNNLMK	627
Db	551	LYPHFRDTVNIASARQLLVAGGVLESTVQSFAMENSAVYKDWFPDQALPADLVK	610
QY	628	RGLAVEDSSAPHGLRLINDYFPAVDGLDIWSAIKTWVQDYCCLYKDDNAVQNDPELOS	687
Db	611	RGVAVEDSSPHGVRLITYEDYPAVDGLEIWSAIKSWVTDYCSFYGSDEILKONELQA	670
QY	688	WNNELREKHADKHEPWPXWQTLSELIESCTTIIMIASHAAVNFQYPGVGVILNR	747
Db	671	WKELEUVGHGDKNEPWPENETPQELIDSCITTIIMIASHAAVNFQYPGVGVILNR	730
QY	748	PTTSRRFMEVGTASYKYLESNPEKAFRLTICSELQALVSTISITIELSKIASDEVYLQOR	807
Db	731	PTVSRREFPEPCTPEYBELKGNPKAFKTTIAQQLILGLSVLEILLSRTTDEIYLQOR	790
QY	808	ASIDWTSDKIALEAEKFGKQLFVENVIRMPERNKEVNLKORSQPVNLPYTLIPVSSNEGL	867
Db	791	ESPEWTKDEPLAADFREGKLTDTIEKQIIQRNGENILTNRSQGVNAPYTLIPVSSNEGL	850
QY	868	TGRGIPNSISI 878	
Db	851	TKGIPNSVSI 861	
RESULT 3			
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ID	LOX1 ARATH	STANDARD;	PRT; 859 AA.
AC	Q0637;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Lipoxygenase 1 (EC 1.13.11.12)		
GN	LOX1 CR AT1G5020 OR F14C21.3 OR F14C21.54		
OS	Arabidopsis thaliana (Mouse-ear cress)		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
NCBI	TaxID=3702;		
RP	[1]		
RP	SEQUENCE FROM N.A.		

STRAIN=cv. Columbia; TISSUE=Root;
MEDLINE=94105302; PubMed=7506426;
Melan M.A., Dong X., Endara K.R., Ausubel F.M.,
Peterman T.K.;
"An Arabidopsis thaliana lipoxygenase gene can be induced by
pathogens, abscisic acid, and methyl jasmonate.";
Plant Physiol. 101:441-450(1993).
[2]
SEQUENCE FROM N.A.
STRAIN=cv. Landsberg erecta;
MEDLINE=94137782; PubMed=8305494;
Melan M.A., Nemhauser J.M., Peterman T.K.;
"Structure and sequence of the Arabidopsis thaliana lipoxygenase 1
gene.";
Biochim. Biophys. Acta 1210:377-380(1994).
[3]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Mafti R., Marziani A.,
Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salsberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Tortumi M.J., Town C.D.,
Utterback T., Van Aken S., Vayenberg M., Vysotskaia V.S., Walker M.,
Wu D., Yu G., Frazer C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.";
RT Nature 408:816-820(2000).
RT
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: BY WOUNDING, ABSICISIC ACID (ABA) AND METHYL JASMONATE.
CC -!- SIMILARITY: Belongs to the lipoxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L04637; AAA32827.1; -;
CC ENBL; U01843; AAA17036.1; -;
CC EMBL; AC069144; AGS1123.1; -;
CC PIR; JQ2267; JQ2267.
CC HSSP; P08170; 2SBL.
CC InterPro; IPR000907; Lipoxygenase.
CC InterPro; IPR01024; Lipoxygenase_LH2.
CC InterPro; IPR008976; PLAT LH2.
CC Pfam; PF00305; lipoxygenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC DR PRINTS; PR00087; LIPOXYGENASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE 1; 1.
CC

Db 4 GGIWDAL--LGKDRPKVKGRVILMKKNVLDIFINIGASVVDGIDLLQKQVSIQLISGV 61
Qy 85 TSNSRGKGVKAYLERLWLTISIPLPAGESVQNFQWD-ENFGPGAFRIKNGHTSEFF 143
Db 62 NYDGLGKLSPAYLESWLTITITAGESVTFVDFWDRDEFVPGAFIKNHLNEFF 121
Qy 144 LKSLTLDVPGVGRVHPCNSWVPSGKRYKDRIFPANHVLPSQTPNPLRKREELWN 203
Db 122 LKSLTLEDVPGVGRVHPCNSWVPSGKRYKDRIFPANHVLPSQTPNPLRKREELWN 181
Qy 204 LRGGTGERKWDRTYDVNDIADPDVGH--RPIILGTTTEYPRRGRTGPRERD 261
Db 192 LRGGTGERKWDRTYDVNDIADPDVGH--RPIILGTTTEYPRRGRTGPRERD 241
Qy 262 HNYSRSLPMSLDIYVVKDENFGLKMSDPLGLTKALSIKIPGLQSFDPVTFNFDN 321
Db 242 PNCESRNLPLMSLDIYVVKDENFGLKMSDPLGLTKALSIKIPGLQSFDPVTFNFDN 301
Qy 322 PKEVDNLPERGFPFPNAP-KTLTDLTPPLFKALVRNDGKFLKPTPEVVKDKNLGWS 380
Db 302 FADVLNLVGGGKILPEGPWLKAITDNISSEILKDIQTDGGLGLKYPTPQVIOGDKTAWR 361
Qy 381 TDEEFARMLAGNPILIRLEAPPTSKLDPNVYGNQNSITTEHIIKHGLDGLTVDEAM 440
Db 362 TDEEFARMLAGNPILIRLEAPPTSKLDPNVYGNQNSITTEHIIKHGLDGLTVDEAM 421
Qy 441 KQNLRIYVDFHMLPXYTRWN-ATSTKYATRLLKDDGTLKPLVIELALPHQGDQ 499
Db 422 KSNRLFIHLHDIWPLLRKINMSANTKAYASRTLLFLQDDRTLKLAIELSLPHPDQDQ 481
Qy 500 LGATSKLFPRAENGVSIMOLAKAYTVNDVGHQHSIHLWHTHVLPEPVIATHROLS 559
Db 482 FGTYSKVTPADQGVGSGIFAKAYAVNDMGHQLISHWHTHVLPEPVIATHROLS 541
Qy 560 VLPHIHLKLVPHYKDTMFINASRQVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQ 619
Db 542 VLPHIHLKLVPHYKDTMFINASRQVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQ 600
Qy 620 ALPNLMKSGLAVEDSSPHGLRLINDYPAVNDGLIWSAIKTVWODYCCLYKDNVAV 679
Db 601 ALPADLKRGAVEDSSPHGLRLINDYPAVNDGLIWSAIKTVWODYCCLYKDNVAV 660
Qy 680 QNDPELQSMNELREKGHADKHPFMPKMTLSIELIESCTTIITWIASALHAANFQYFP 739
Db 661 EKDTLOAWKRELREEGHGKDEAWPKLQTRQELDCCTIITWIASALHAALHFLGLS 720
Qy 740 YGYILNPPTSRPMPVGTAYKELESNEPEKAPLRTICSEALQVSIHIIELSKHAS 799
Db 721 YAGYLPNRPITSCNLMPEPGSVYEELKTNPKVFLKTFVPLQSLLEISIFVSSRSHAS 780
Qy 800 DEVYLGQASIDWTSKLTALBAFKFGKLPVENRWERKEVNLKRNKSGPNVLPYTL 859
Db 781 DEVYLGQASIDWTSKLTALBAFKFGKLPVENRWERKEVNLKRNKSGPNVLPYTL 840
Qy 860 VPSNNEGTLGRGIPNSISI 878
Db 841 PPTSEGLTGKIPNSVSI 859

RESULT 5

LOX3_SOYBN STANDARD; PRT; 857 AA.
AC F09186; Q39838;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase-3 (EC 1.13.11.12) (L-3).
GN LOX1.3 OR LOX3.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;

RN SEQUENCE FROM N.A.
RP Yenofsky R.L.; Fine M., Liu C.;
RT Isolation and characterization of a soybean (Glycine max)
RT lipoxigenase-3 gene.;
RL Mol. Gen. Genet. 211:215-222(1988).
RN [2]
RP REVISIONS.
RA Yenofsky R.L.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASN-713.
RC STRAIN=cv. Provar;
RX MEDLINE=95092758; PubMed=7999759;
RA Kramer J.A., Johnson K.R., Dunham W.R., Sands R.H., Funk M.O. Jr.;
RT "Position 713 is critical for catalysis but not iron binding in
RT soybean lipoxigenase 3";
RL Biochemistry 33:15017-15022(1994).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=cv. Provar;
RX MEDLINE=97440646; PubMed=9294864;
RA Skrzypczak-Jankun E., Anzel L.M., Kroa B.A., Funk M.O. Jr.;
RT "Structure of soybean lipoxigenase L3 and a comparison with its
RT L1 isoenzyme";
RL Proteins 29:15-31(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=cv. Provar;
RX MEDLINE=99119225; PubMed=9922163;
RA Pham C., Jankun J., Skrzypczak-Jankun E., Flowers R.A., Funk M.O. Jr.;
RT "Structural and thermodynamic characterization of lipoxigenase-
RT catechol complexes";
RL Biochemistry 37:17952-17957(1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=cv. Provar;
RX MEDLINE=21547069; PubMed=11686682;
RA Skrzypczak-Jankun E., Bross R.A., Carroll R.T., Dunham W.R.,
RA Funk M.O. Jr.;
RT "Three-dimensional structure of a purple lipoxigenase";
RL J. Am. Chem. Soc. 123:10814-10820(2001).
CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENSATION OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienate.
CC -1- COFACTOR: Iron, one atom tightly bound per molecule.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56928; CAA30016.1; -
DR EMBL; X13302; CAA31664.1; ALT_SEQ.
DR EMBL; USC081; AAB41272.1; -
DR PDB; 1LNH; 29-MAR-96.
DR PDB; 1N03; 03-JUN-03.
DR PDB; 1IK3; 14-NOV-01.
DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXIGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXIGENASE_1; 1.
DR PROSITE; PS00081; LIPOXIGENASE_2; 1.
DR PROSITE; PS00955; PLAT; 1.
KW Oxidoreductase; Dioxigenase; Iron; Multigene family; 3D-structure.
FT DOMAIN 38 163
FT METAL 518 518
FT METAL 523 523
FT METAL 709 709
FT METAL 857 857
FT METAL 857 857
FT VARIANT 25 25
FT VARIANT 57 57
FT VARIANT 112 112
FT VARIANT 201 201
FT VARIANT 382 382
FT VARIANT 428 428
FT VARIANT 630 630
FT MUTAGEN 713 713
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FT STRAND 11 20
FT HELIX 21 24
FT TURN 26 28
FT HELIX 29 31
FT HELIX 50 54
FT TURN 55 57
FT STRAND 58 64
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FT STRAND 85 86
FT TURN 89 91
FT TURN 94 95
FT STRAND 96 104
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FT STRAND 112 119
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FT HELIX 357 359
FT HELIX 361 370

FT STRAND 379 379
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FT TURN 391 394
FT STRAND 398 398
FT TURN 403 404
FT HELIX 415 420
FT TURN 421 422
FT STRAND 424 428
FT TURN 431 433
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FT HELIX 554 564
FT TURN 565 565
FT TURN 568 569
FT HELIX 571 575
FT TURN 577 578
FT HELIX 579 581
FT HELIX 582 590
FT TURN 591 592
FT HELIX 595 598
FT HELIX 600 606
FT TURN 607 608
FT STRAND 610 612
FT TURN 614 615
FT TURN 617 618
FT STRAND 620 622
FT TURN 625 626
FT HELIX 628 649
FT TURN 650 651
FT HELIX 655 659

Query Match 59.2%; Score 2769; DB 1; Length 857;
Best Local Similarity 60.0%; Pred. No. 5e-181;
Matches 521; Conservative 132; Mismatches 184; Indels 32; Gaps 7;
QY 28 GNILDRVSSLGNKIKGVILMRSNVLDPTEFHS-----NLLDNFTLGGG 74
DB 3 GGLLHR-----GHKIKGTIVLMRKVNLHVNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRP 57
QY 75 VSFQLISATHSTNSDRGKVGKNKAYLERWLTSTIPPLFAGESVFCINFORNFQDENFGPPGAPFI 134
DB 58 VSLQLISATKADANGKGLGKATFLEGIITSLTLGAGQSAFKINFENDDSGILGAFYI 117
QY 135 KNIGHTSEPLKSLTLDVPGYGRVHFDCNSWYPSGRYKDKRIFFANHVYLPSTQPNPLR 194
DB 118 KNFMQTEFFLVSLTLEDIPNHGSIHFVCSNWIYNAKLFKSDRIFFANQTYLPSETPAPLV 177
QY 195 KYRBEELNLRGDTGERKEWDRIYDYVDYNDIADPDVGDH--REILGGTTEYPYPRGR 252
DB 178 KYRBEELNLRGDTGERKEWERYDYVDYNDLGDPDGKGENHARVPLGNDTFFPYPRGR 237
QY 253 TGRPRSRDHNYESRLSPIMSLDIYVPKDFNGHFKMSDFLGYTLKALISIKPLQSQIF 312
DB 238 TGRKPTRKDPNSES-----SNDVYLPRDEAFGLKSSDFLTGLKSVSNVLPLOSAP 292
QY 313 DV--TNEFDNPKEDYNLFERGFPIPFNAFKTLTDLTP-PLFKALVENDGCKFLKPTTP 369
DB 293 DLNFTPREFDSFDEVHGLYSGGIKLPD-----ITSKISPLFVLKELFRTDGEQALKFPFP 346
QY 370 EYVKONKIGWSTDEBFAREMLAGPNPLIRLEAPPTSKLDPNVYGNQNSTITEEHKH 429

Db 482 GDKSGFVSKVILPADEGVESTIWLAKAYVVVNDSCYHQLMSHLNTHAVIEPVIATNR 541
 Qy 557 QLSVLHPTKILVPHVKTMP- INASARQVLINANGLIETHYPSKYSMELSLTYKDW 615
 Db 542 QUSVHPINKLAPHYRDTMMINALARDSLINANGLIERSFLSKYAVEMSSAVYKVV 601
 Qy 616 PPDQALPNLMKRGIAVEDSSAPHGLRLINDYPAVDGLDIWAISAKTWODYCCLYK 675
 Db 602 FTDQALPNDLIKRNMAVSSSPYGLRLIEDYPYAVDGLBIWTAIKTWQDYVSLYAT 661
 Qy 676 DNAVONDELQSWNELBKGADKXHEPWPWKOTSELIESCTTIWITASALHAANVF 735
 Db 662 DNDIKNDSELOHWKEVVEKGHGLDKDPWPKQTDFDELVECTTIWITASALHAANVF 721
 Qy 736 GQPYGGVILNPTTSSRFMPVEGTAAYKELESNPERKAFRTICSELQALVSIIBILS 795
 Db 722 GQPYGGVILNPTLRRLLPEEGTAEDYEMVKSSQKAYLATITPKQTDLDSVIBILS 781
 Qy 796 KHASDEVILQPASIDWTSDKIALBAPFKGNLFVENRIMERKVENLKNRSGPNLP 855
 Db 782 RHASDEVILQRENPHWTSDSKALQAFQFGNKLAEIEAKLTNKNOPSLYHRYGVPQLP 841
 Qy 856 YTLVFPSSNEGLTGRGIENSISI 878
 Db 842 YTLHPSSKEGLTFRGIENSISI 864

RESULT 7
 Lox3 PEA
 ID Lox3 PEA STANDARD; PRT; 861 AA.
 AC P09518;
 DT 01-VAR-1989 (Rel. 10, Created)
 DT 01-VAR-1989 (Rel. 10, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Seed lipoxigenase-3 (EC 1.13.11.12).
 GN LOX1.3.
 OS Pism sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OC NCBI_TaxID=3888;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Brite;
 RX MEDLINE=89025643; PubMed=3140791;
 RA Baling P.M., Casey R.;
 RT The complete amino acid sequence of a pea (Pisum sativum) seed
 RL lipoxigenase predicted from a near full-length cDNA.";
 RL Biochem. J. 253:915-918(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Brite;
 RA Casey R.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 CC hydroperoxyoctadeca-9,11-dienoate.
 CC -!- COFACTOR: Iron.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; X07807; CAA30666.1; -;
 DR EMBL; X78581; CAA55319.1; -;
 DR PIR; S01142; S01142.
 DR HSSP; P03186; L1NH.
 DR InterPro; IPR00907; Lipoxigenase.
 DR InterPro; IPR001024; Lipoxigenase_LH2.
 DR InterPro; IPR008976; PLAT_LH2.
 DR Pfam; PF00305; lipoxigenase; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; P00087; LIPOXYGENASE.
 DR SMART; SM00308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE; PS00881; LIPOXYGENASE_2; 1.
 DR PROSITE; PS00951; PLAT; 1.
 KW Oxidoreductase; Dioxigenase; Iron; Multigene family.
 FT DOMAIN 41 166
 FT METAL 522 522
 FT METAL 527 527
 FT METAL 713 713
 FT METAL 861 861
 SQ SEQUENCE 861 AA; 97628 MW; 442510278225D750 CRC64;
 Query Match 57.7%; Score 2696.5; DB 1; Length 861;
 Best Local Similarity 58.3%; Pred. No. 4.4e-176;
 Matches 506; Conservative 145; Mismatches 184; Indels 33; Gaps 7;
 Qy 30 ILDRVSSLGNGIKGKIVLMRSNVLDFT-----EFHNLNDNTTELLGGVS 76
 Db 8 ILNR-----GHKIKGTIVLMRKXNVLDSLTAVGGVIGQGFILGSTVDNLTAFGRSVS 62
 Qy 77 FOLISATHTSNDGRGKGNKAYLERWLSIPPLPAGESVQINFDWENFGFPGAFFIKN 136
 Db 63 LQLISATKPDATGKGLGKATLEGLISLPLGLGQSAFKLHFDDMDGIPGAFYIKN 122
 Qy 137 GHTSEFFLSLTLDVPGYGRVHPCSNWVPSGYSKKDRIPFANHYVLPQTPNPLKY 196
 Db 123 FMQTEFFVSLTLDIPNHGSIYFVCSNWIYNAHKIKIDRIPFANQTYLPSETPAVLVY 182
 Qy 197 REELWNLRGDTGKERKEDRIYDVNDIADPDVGDH--RPILGGITEYPPRRGTG 254
 Db 183 REELNLRGDTGKERKEDIYDVNDLGNPSGHNHARPVLGGSETTYPPRRGTG 242
 Qy 255 RPRSRDHNYESRLSPIMSLDIYVPKDNFNGHKLMSDFGLYTLKALSISIKPGLSIF-- 312
 Db 243 RXPTRKDPNSESER-----SDYVYLRDEAFGLKSSDFLYGLKAVSQNVVPALESVFFD 297
 Qy 313 -DVTPNEFDNFKEVNDLPERGPIFPNAPKLTEDLTP-PLFKALVRNDGEKFLKFTPE 370
 Db 298 LNFTEPNEFDSFDEVHGLYEGGKILPTN-----ILSQISPLVLKEIFRTDGTNTLYPPPK 353
 Qy 371 VVKDNKIGSTDEEFAREMLAGNPILLIRLEAFPTKLDPNVYGNQNSITTEHIIKHG 430
 Db 354 VTQVSSGHWMTDEEFAREMLAGNVNVCCLQEFFPRSKLDSQIYGDHTSKISKEHLEPN 413
 Qy 431 LDGLTVDEAMKQNRLYIVDFHDLAMPYTRMNATSKTYATRTLLLLKDDGTLKPLVIEL 490
 Db 414 LEGLATVEEAIONKQLFLLDHDSIMPYLRRINSTKAYATRTILFLNNQNLKELATEL 473
 Qy 491 ALPHPGDGLGALSILYRPAENGVSQWQLAKAYVVDVNDVGYHQLISHWLHTHAVLEPP 550
 Db 474 SLPHPGDDEHGAIVSYVQPALEGVSSWLLAKAYVINDSCYHQLVSHLWTHAVLEPP 533
 Qy 551 VIATHRQLSVLHPHKLVLPHYKDTMTFINASARQVLINANGLIETHYPSKYSMELSSIL 610
 Db 534 VIATNRHLSCLHPIYKLLYPHYRDTMNINSLARSLVNDGGIIEKTFWLGWYMEMSSKY 593
 Qy 611 YKDWTFPDALPNMLKGLAVEDSSAPHLRLINDYPAVDGLDIWAISAKTWQDYVCC 670
 Db 594 YKNWVTEQALPADLIKRGNALEDSSPGVKLVVDEPIYAVDGLLEIWAIKTWQDYVS 653
 Qy 671 LYKDKDNAYQNDFELQSWNELREKGHADKKHEPWPWKQOTLSIELIESCTTIWITASALH 730

Db 654 LYTSDEKLQDSSELOAWKELVEVGHGDKQNEPWPQMQTRDLEIVCSIVITWASALH 713

QY 731 AAVNGQPYGYILNRPTRRRFMEVGTATYKELESNPKAFRLTICSELOALVSISI 790

Db 714 AAVNGQSYGGLIILNRPTRRRFMEVGTATYKELESNPKAFRLTICSELOALVSISI 773

QY 791 LEILSKHASDEVYLGORASIDWTSKIALEAFKFGKULFEVENRIMERNEVNLKRSRG 850

Db 774 LEILSKHASDEVYLGORASIDWTSKIALEAFKFGKULFEVENRIMERNEVNLKRSRG 833

QY 851 PVNPLYTLVPSSNEGLTGRGIPNSISI 878

Db 834 PVEMPYTLVPSSKEGLTFRGIPNSISI 861

RESULT 8

LOX2 SOYBN STANDARD; PRT; 865 AA.

ID LOX2 SOYBN STANDARD; PRT; 865 AA.

AC P09439;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Seed lipoxigenase-2 (EC 1.13.11.12) (L-2).

GN LOX1.2 OR LOX2.

OS Glycine max (Soybean).

OC Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

OX NCBI_TaxID=3847;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88198254; PubMed=2834391;

RA Shibata D., Steczko J., Dixon J.E., Andrews P.C., Hermodson M.,

RA Axelrod B.;

RT "Primary structure of soybean lipoxigenase L-2.;"

RL J. Biol. Chem. 263:6816-6821(1988).

RN [2]

RP SEQUENCE OF 231-865 FROM N.A.

RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,

RA Altschuler M.;

RT "Two soybean seed lipoxigenase nulls accumulate reduced levels of lipoxigenase transcripts.;"

RL Plant Mol. Biol. 7:11-23(1986).

CC -!- FUNCTION: PLANT LIPOXIGENASE MAY BE INVOLVED IN A NUMBER OF DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS, CIS-1,4-PENTADIENE STRUCTURE.

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13E)-13-hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron, one atom tightly bound per molecule.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES, L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 691 TO 865 DUE TO A FRAMESHIFT.

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CC -----

CC EMBL; J03211; AAA33987.1; .

DR F01; A28161; DASYL1.

DR HSP; P08170; 2SBL.

DR InterPro; IPR000907; Lipoxigenase.

InterPro; IPR001024; Lipoxigenase_LH2.

DR InterPro; IPR008976; PLAT_LH2.

DR Pfam; PF00305; lipoxigenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PRO0087; LIPOXIGENASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXIGENASE_1; 1.

DR PROSITE; PS00081; LIPOXIGENASE_2; 1.

DR PROSITE; PS00095; PLAT; 1.

KW Oxidoreductase; Dioxigenase; Iron; Multigene family.

FT METAL 50 175

FT METAL 527 527 IRON (BY SIMILARITY).

FT METAL 532 532 IRON (BY SIMILARITY).

FT METAL 718 718 IRON (BY SIMILARITY).

FT METAL 865 865 IRON (BY SIMILARITY).

FT CONFLICT 263 264 KP -> NL (IN REF. 2).

FT CONFLICT 313 313 D -> Y (IN REF. 2).

FT CONFLICT 400 400 L -> P (IN REF. 2).

FT CONFLICT 428 428 L -> H (IN REF. 2).

FT CONFLICT 485 486 D -> G (IN REF. 2).

FT CONFLICT 502 502 V -> G (IN REF. 2).

FT CONFLICT 534 534 V -> L (IN REF. 2).

SQ SEQUENCE 865 AA; 97145 MW; 74CBD32E3E4A0C85 CRC64;

Query Match 57.5%; Score 2690; DB 1; Length 865;

Best Local Similarity 58.4%; Pred. No. 1.2e-175;

Matches 513; Conservative 127; Mismatches 194; Indels 44; Gaps 8;

QY 23 VINAGNILDVRSSLGNGKIKGVILMRSNVLDPTEFH-----SNLL 64

Db 10 ILNRG-----GGHKIKGTIVLMRKNVLDNFNSVADLTGKNGVGLTGTGLNVGVSTL 59

QY 65 DNFTELLGGVSPOLISATHTSNDRGKVGKAYLERWLTSTPPLFAGESVQINFWDE 124

Db 60 DNLTAFLGRSVALQLISATKPLANGKRGVKGTFTLEGIIVSPTTGAGESAFNIOFEMDE 119

QY 125 NFGFPGAFFIKNGHTSEFFLKSLTLDVPGYGRVDFDCNSWYPPGKRYKDKRIFANHY 184

Db 120 SMGIPGAFYIKVMQVEFYLSLTLEDVFNQGTIRFCVNSWYVNTKLYKSVRIFANHY 179

QY 185 LPSQTNPLRKYREBELNLRGDTGERKEWRIYDYVDYNDIADPDVGDH--RLIGST 242

Db 180 VPESETPAALVGREBELKNLRGDTGERKEHRIYDYVDYNDLGNPDHGFENFARLILGS 239

QY 243 TEYPPRRGRTGRPSRRDHNYESRLSPIMSDIYVVDKDNFGLKMSDFLYTKALSI 302

Db 240 SHYPYRRGRTGRYPTRKDNSEK-----PGEVYVPRDNEFGLKSSDFLAYGKLSQ 293

QY 303 SIKPGIQSIFDV--TPNEFDNKEVDNLPFERGPIPTFNAKTLTDLTPPLFKALVRNDG 360

Db 294 YVLPAPESVFDLNTFNEPFDSPQVDRDLHEGGIKLPTEVISTI---MPLPVYVKELFRTDG 350

QY 361 EKFLKPEPTPEVYKDNKIGWSTDEEFAREMLAGPNLLIRLEAFPTSKLDENVYGNQS 420

Db 351 EQVLKPEPPPHVIOVSKSAMWTDDEEFAREMVGVCVINGLQEPFKSNLDTTIVGEQTS 410

QY 421 TITEEHKGLDGLTVEAMQNRLIYVDFHDALMPYLTRMNATSTKYATRTLLKDD 480

Db 411 KITADAL--DLGGYTVDEALSGRLFMLDYHDFVFNPIRRINQTVAKAYATRTILFLRN 468

QY 481 GTLKPLVIELAPHPQGDOLGAISKLYPPEANGVOKSIMOLAKAYVNDVYHOLISHW 540

Db 469 GTLKPLVAIELSPHPAGDUSGAVSQVILPAKEGVSTIMLLAKAYVNDVYHOLISHW 528

QY 541 LHTHAVLEFPVATRRQLSVLHPHKLVLPHYKDMFMINASARQVLINANGLIETHVPS 600

Db 529 LANTHAVIEFPFIATNRHLSALHPYIKLLTPHYRDTMNLARQSLINADGIIKSFUPS 588

QY 601 KYSMELSSILYKDWTFPPDOALPNMLKRGVLAEDSSAPHLRLLINDPFAVDGLDINSA 660

Db 589 KHSVEMSSAVYKNWVFTDQALPADLTKRGVAIKPSAPHLRLLIEDYPYAVDGLGEIWA 648

QY 661 IKTWQDYCYCLVYKDDNDVQNDPFLQSWWNLREKGHADKKHEPWWPKMQLSELIESCT 720

Db 649 IKTWQEVSLYYARDVDDKSELOQWKAWEKGGDLKKDPWPKLQIEBLVICT 708
QY 721 TIWIASALHAANVFGQYGYILNRPTTERRFMPEVGTAYBYKELSNPKAFRLRTICS 780
Db 709 IITWIASALHAANVFGQYGYILNRPTTERRFMPEVGTAYBYKELSNPKAFRLRTICS 768
QY 781 ELQALVSIITILSKSHASDEVYLGORASIDWTSKTALEAFKFKGNLFEVENRIMERN 840
Db 769 KFTQVLDUSVIELRHASDEVYLGORNDPHWTSKALQAPQKFGNKLKEIEKAKRN 828
QY 841 KEWNLKNSGPNVLYTYLLVFNSSNGLTGRGIPNSISI 878
Db 829 NDOSLNRLGVPQLPYTYLLHNS-EGLTGRGIPNSISI 865

RESULT 9
LOXX SOYBN
ID LOXX SOYBN STANDARD; PRT; 864 AA.
AC P24095;
DT 01-WAR-1992 (Rel. 21, Created)
DT 01-WAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase (EC 1.13.11.12).
GN LOX1.4 OR SC514.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxId=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=91370880; PubMed=1909908;
RA Shibata D., Kato T., Tanaka K.;
RT "Nucleotide sequences of a soybean lipoxigenase gene and the short
intergenic region between an upstream lipoxigenase gene.";
RL Plant Mol. Biol. 16:353-359 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams 82; TISSUE=Radicle;
RA Park T., Holland M.A., Laskey J.G., Polacco J.C.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: GERMINATED COTYLEDONS.
CC -!- INDUCTION: By jasmonate.
CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.

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or send an email to license@isb-sib.ch).

DR EMBL; X56139; CAA39604.1; -;
DR EMBL; U04526; AAA03728.1; -;
DR PIR; S13381; S13381.
DR HSP; P08170; 2SBL.

DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PRO0087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase; Lipoxigenase; Iron; Multigene family.
FT DOMAIN 44 171
FT METAL 525 525 IRON (BY SIMILARITY).
FT METAL 530 530 IRON (BY SIMILARITY).
FT METAL 716 716 IRON (BY SIMILARITY).
FT METAL 864 864 IRON (BY SIMILARITY).
FT CONFLICT 233 233 S -> C (IN REF. 2).
FT CONFLICT 240 240 R -> L (IN REF. 2).
FT CONFLICT 604 604 D -> H (IN REF. 2).
FT CONFLICT 695 695 M -> K (IN REF. 2).
SQ SEQUENCE 864 AA; 96816 MW; 66F31PB1FA5F3B60 CRC64;

Query Match 56.6%; Score 2644.5; DB 1; Length 864;
Best Local Similarity 58.1%; Pred. No. 1.6e-172; Indels 37; Gaps 7;
Matches 504; Conservative 125; Mismatches 201;

QY 39 GNKIGKGVILMSNVLDTEPHS-----NLLDNFTLGGGVS 76
Db 8 GQKIGTVLMPKPNVLDFAITSIGKGVVDITATGILQGVSLVGGVIDTATSLGRNIS 67
QY 77 FOLISATHTSNDGRGVGNKAYLERWLTISIPLFAGESVFOINQWDFNFGPGAFFKN 136
Db 68 MQLISATQTDGSGNGKGVKVEYLEKHLPTPLTGLARQDAFSIFFEWDASFGIPGAFYKN 127
QY 137 GHTSPFFKSLTLDVDPVGRVHFDNSWVPSGRYKDKRIFPFANHVLPSTQNPRLKY 196
Db 128 FMTDSEFLVSKLEIDPNHGTFIEVCNSWVNFYSYKKNRIFVNDVTLPSATPAFLKY 187
QY 197 REELNLRGDTGERKWDRIYDVNDIADPVGDHRPILGTTGTPYPRRGTORP 256
Db 188 RKEELEVLRGDTGRKDFRIYDVNDVNDLGNPDGDPRLPGSSIVYPRRVRTORE 247
QY 257 RRRDHNTESRLSPIMSLDIYVVKDENFCHLQMSDFLGVTLKALISIKPGLOS-IFD-- 313
Db 248 RRTDPNSEK-----PGEVYVPRDENFCHLQMSDFLGVTLKALISIKPGLOS-IFD-- 301
QY 314 VTPNEFDNPFVDNLFERGFPIPFNAFKTLTDLTP-PLFKALVNDGKELKFPTEPV 372
Db 302 VTSSEFSESPEDVRSLYEGGKILPTD-----ILSQISPLPALKEIFRTDGENVLQFPFPHVA 357
QY 373 KDKKIGWSTDEEFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNSTITEEHKGLD 432
Db 358 KVSXGMMWDEEFAREVIAGVNFVIRLQEPFPPKSTLDPTLYGDTSTIINEKEINWG 417
QY 433 GLTVDEAMKQNLRIYVDFHDMALPILTRMNTATST-KTYATRLLLKDDGTLPKLVIELA 491
Db 418 GVTVEEALSTQRLFDLYQDAFIPVLTIRINSLPTAKAVATRIILFKDDGTLPKLVIELS 477
QY 492 LPHPOGDQIGALSKLYFFAENGQVKSINQLAKAVYVNDVGHQILSHWLTHAVLEPV 551
Db 478 KPHPPGDNLGPESIVVLVATEGVDSITWLLAKAHVINDSGYHQVLVSHWLTHAVNSPFA 537
QY 552 IATHPQLSVLHPIHKLVLPHYKDTMFINASARQVLINANGLTETHTYPSKYSMESSILY 611
Db 538 IATNRHLSVLHPIYKLLVPHYEDTININGLAQSLINADGIERKSLFGKYSIEMSSSV 597
QY 612 KDWTFPDQALPNLMKRGIAVEDSSAPHLRLINDYFPAVDGLDINSATWQDYDQCL 671
Db 598 KMWVFTDQALPADLVKRGIAVEDSPAPHLRLINDYFPAVDGLDINSATWQDYDQCL 657
QY 672 VYKDDNAVONDELOSWMNELREKHADEKPEWPKMQLSELTSETTIIWIASALHA 731
Db 658 YFPTDAAVQDDTELOAWKWEKGGDLKKEPKWPKMQLSELTSETTIIWIASALHA 717

QY 732 AVNFGQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFIATICSLOALVSI 791
 Db 718 AVNFGQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFIATICSLOALVSI 777
 QY 792 EILSHASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKENVNKNRSGP 851
 Db 778 EILSHASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKENVNKNRSGP 837
 QY 852 VNLPTVLLVPSNEGLTGRTGIPNSISI 878
 Db 838 VOLPPTVLLVPSNEGLTGRTGIPNSISI 864

RESULT 10
 LOXA PHAVU
 ID LOXA PHAVU STANDARD; PRT; 862 AA.
 AC P27480;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipoxigenase 1 (BC 1.13.11.12).
 GN LOXA OR LOX1
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 OX NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=sv. Red Mexican; TISSUE=Leaf;
 RX MEDLINE=94171713; PubMed=8130796;
 RA Eiben H.G.; Slusarenko A.J.;
 RT "Complex spatial and temporal expression of lipoxigenase genes during
 Phaseolus vulgaris (L.) development.";
 RL Plant J. 5:123-135 (1994).
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 DEVELOPMENT, PEST RESISTANCE, AND SENSITIVE OR RESPONSES TO
 WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
 A CIS, CIS-1,4-PENTADIENE STRUCTURE.
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 hydroperoxyoctadeca-9,11-dienoate.
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X63525; CAM45088.1; -.
 DR F01; S22153; S22153.
 DR HSBP; P08170; 2SBL.
 DR InterPro; IPR000907; Lipoxigenase.
 DR InterPro; IPR001024; Lipoxigenase_LH2.
 DR InterPro; IPR008976; PLAT_LH2.
 DR Pfam; PF00305; lipoxigenase; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; PR00087; LIPOXYGENASE.
 DR SMART; SM00308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE; PS00095; PLAT; 1.
 KW Oxidoreductase; Dioxigenase; Iron; Multigene family.
 FT DOMAIN 44 171
 ID Lox4_SOYBN PLAT.
 FT METAL 522 522 IRON (BY SIMILARITY).

FT METAL 527 527 IRON (BY SIMILARITY).
 FT METAL 713 713 IRON (BY SIMILARITY).
 FT METAL 862 862 IRON (BY SIMILARITY).
 SQ SEQUENCE 862 AA; 97154 MW; 24566DICEE3C191E CRC64;
 Query Match 55.5%; Score 2596; DB 1; Length 862;
 Best Local Similarity 56.7%; Pred. No. 3.2e-169; Indels 42; Gaps 9;
 Matches 496; Conservative 142; Mismatches 195;
 QY 30 ILDRVSSLOGNKIKGVILNRNSVLDFTFEHSS-----NLLDNF 67
 Db 4 ILNR-----GHKIKGTWLMVTKNVDENEFVSTTRGGIVGAAGGLFGAATDIVGGIVDGA 58
 QY 68 TELGGGVSVFOLISATHSTNSRGKVKYKAYLERWLTSTIPPLFAGESVFOINFDENFG 127
 Db 59 TAIFSRNIAIQLISATKTDLGLNGKVGKQTFLFKHLPSLNLGDRQDAFNVFVFEWDENFG 118
 QY 128 FPGAFFIKNGHTSEFFFLKSLTLDVPGYGRVHFDCNSWVYPSGRYKGRKRIFFANHVLP 187
 Db 119 IPEAFYIKFMQSEFFFLVSLTLEDIPNHGCTIHFCVNSWYNAKSKYKDRIFANKTYLPN 178
 QY 188 QTENPLKRYREBELWNLRGDGTGERKEWRIYDYVDYNDIADPDVGDH--RPILGSTTY 245
 Db 179 ETPASLVKRYKELENLRGDTGERKEYDRIYDYVYNDLGNPKNKNLARTTLGSSDF 238
 QY 246 PYPRRGRTGKPRRRDHNYESRLSPIMSLDIYVPKDENFGHLKMSDFLGYTLKALSISTK 305
 Db 239 PYPRRGRTGKSTRDKPCKE-----IPTSDTIPDENFGHLKSGDFLYAIKSLTONVL 293
 QY 306 PGLQSIQFDVTPNEFDNFKVDNLFERGFPIPPNAPFKTLTDTPLPKALVRNDGKFLK 365
 Db 294 PTFQKAFGN-NEFDTFEDVGRGLFEGGLYLPDTSKIS--PIPVKELIATDGEQVLK 349
 QY 366 FTEPVEVVDNKGKMSDEFEAFEMLAGNPLIRLEAPPTSKLDPNVGNQNTIIEE 425
 Db 350 FPPHVRVTKSAMTDEEFREMGELAGVNPCLIQRLQSEFPKSKLDVTVYGDSTMTK 409
 QY 426 HKHGDGLTVDKAMQNRLYIVDFHDALMPYLTMNATST-KTYATRTLLLLKDDGLTK 484
 Db 410 HLEINLGLTVEALHGNRFLFDHDAFIPYLERINDLPYAKVATRTILFKDDNTLK 469
 QY 485 PLVIELALPHQDQGLGALSILYKLYFAENGQVKSILQALAKAYTVNDVGVHQLISHWLTH 544
 Db 470 PLAIELSLPNPGK--GANSRVILPADGGAESTIWLAKAYVYVNDSCYHQLMSHLNTH 527
 QY 545 AVLEPEVIATHRQLSVLHPHKLPHYKDTMFINASQVLINANGLIETTHYPSKYSM 604
 Db 528 AVNEPVIATNRHLSVLHPHKLPHYEDTWNIALARQSLINAGGVIERSFLEGEFV 587
 QY 605 ELSSILYKDWTPDQALPNLMKRGVAVEDSSAPHLRLINDYFVAVDGLDIWSAITSW 664
 Db 588 EMSAVYKSWVFTDQALPADLIRKGMVAVEDPSSPYGLRVVSDYFVAVDGLDIWDTIQTW 647
 QY 665 VODYCLLYKDDNAVQNDPELOSWNELREKHAQKHEPWPMPKQTLSELIESCTTIW 724
 Db 648 VKDYVSLYPTNDVAKKOTELQAWKEAVEKGHGLKDKPMPKQTLSELIESCTTIW 707
 QY 725 IASALHAAVNFQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFIATICSLOA 784
 Db 708 IASALHAAVNFQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFIATICSLOA 767
 QY 785 LVYSISIIETLSKASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKENVN 844
 Db 768 IVDLSVIELSRHASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKENVN 827
 QY 845 LKNRSGPVNLPYLLVPS--SNEGLTGRGIPNSISI 878
 Db 828 LKNRSGPVNLPYLLVPS--SNEGLTGRGIPNSISI 862

RESULT 11
 LOX4_SOYBN
 ID Lox4_SOYBN STANDARD; PRT; 853 AA.

P38417;
 01-OCT-1994 (Rel. 30, Created)
 01-OCT-1994 (Rel. 30, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipoxigenase-4 (FC 1.13.11.12) (L-4) (VSP94).
 GN LOX1.5 OR LOX4.
 OS Glycine max (soybean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 CC NCBI_TaxID=3847;
 RN [1]_TaxID=3847;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Enrei;
 RA Kato T., Shirano Y., Iwamoto H., Shibata D.;
 RT "Soybean lipoxigenase L-4, a major component of the 94-kilodalton
 RT storage protein in vegetative tissues: expression and accumulation in
 RT leaves induced by pod removal and by methyl jasmonate.";
 RL Plant Cell Physiol. 34:1063-1072(1993).
 RN [2]
 RP PARTIAL SEQUENCE.
 CC TISSUE=Cotyledon;
 RA Kato T., Ohta H., Tanaka K., Shibata D.;
 RT "Appearance of new lipoxigenases in soybean cotyledons after
 RT germination and evidence for expression of a major new lipoxigenase
 RT gene.";
 RL Plant Physiol. 98:324-330(1992).
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENSITIVE OR RESPONSES TO
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 CC hydroperoxyoctadeca-9,11-dienoate.
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: FOUND IN MATURING AND DEVELOPING SEEDS. IN
 CC YOUNG SEEDLINGS IT IS FOUND IN COTYLEDONS, HYPOCOTYLS, ROOTS AND
 CC PRIMARY LEAVES.
 CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED. EXPRESSION IS HIGH
 CC 3 TO 5 DAYS AFTER GERMINATION AND RETURNS TO BASAL LEVEL BY DAY 9.
 CC -!- INDUCTION: BY POD REMOVAL AND METHYL JASMONATE.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: D13999; BAB03101.1;
 CC EIR; T07662; T07662.
 CC HSP; P09186; ILNH.
 CC InterPro: IPR000907; Lipoxigenase.
 CC InterPro: IPR01024; Lipoxigenase_LH2.
 CC InterPro: IPR008976; PLAT_LH2.
 CC Pfam: PF00305; lipoxigenase; 1.
 CC Pfam: PF01477; PLAT; 1.
 CC PRINTS: PR00087; LIPOXYGENASE.
 CC SMART; SM00308; LH2; 1.
 CC PROSITE; PS00711; LIPOXYGENASE_1; FALSE_NEG.
 CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
 CC PROSITE; PS00095; PLAT; 1.
 CC Oxidoreductase; Dioxxygenase; Iron; Multigene family.
 CC DOMAIN 34 159 PLAT;
 CC FT METAL 513 513 IRON (BY SIMILARITY).
 CC FT METAL 518 518 IRON (BY SIMILARITY).
 CC FT METAL 704 704 IRON (BY SIMILARITY).
 CC FT METAL 853 853 IRON (BY SIMILARITY).

SQ SEQUENCE 853 AA; 96534 MW; 533175EE1CFB34FC CRC64;

Query Match 55.4%; Score 2591; DB 1; Length 853;
 Best Local Similarity 57.4%; Pred. No. 6.9e-169;
 Matches 492; Conservative 133; Mismatches 204; Indels 28; Gaps 10;

QY 39 GNKIKGKVLMSNVLDFTFHS--NLADNFTFLGGV-----SQILSATHTS 86
 DB 8 GQKIKGTVVMQKNVLDINSITVSGVQDGLGFGSAVDALTFAATKISQLSAT-KA 66
 QY 87 NDSRGKVGKAYLERWLTSIPDLFAGESVQINFQWENFGPPGAFKINGHTSEFFLKS 146
 DB 67 DGGKGIKGSTNLRGKIT-LPTLGAGEQAYDNFWDSDFGIPGAFYIKNFQWFEYLKS 125
 QY 147 LTLDDVPGVGRVHFDGNSWVPSGYKQRIFFANHVLPSTQNPPLKRYEELNLNRG 206
 DB 126 LILEDPINRHTTHFCVNSWVNSKNYKTRIPFANNYLPSETPAPLKRYEELNLNRG 185
 QY 207 DGTGERKEWDRIYDYVDVNDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPRRDHNY 264
 DB 186 DGTGERKEWDRIYDYVDVNDLGNPDGKYARFVLGSSA-LPYPRERTGRKTRKDPNS 244
 QY 265 ESRLSPIMSLDIYVPKDNFGLKMSDFGLYTLKALSISIKFGLQSIID--VTPNEPNNF 322
 DB 245 EK-----PSDFVYLPDEAFGLKSSDFLAYIKSVSDVLPVLDADFGLNLSLEPNNF 299
 QY 323 KEVDNLFERGFPPIPNFAFKTLTDLTPPLFKALVNDGKFKLFTPEVVKDKNIGWSTD 382
 DB 300 AEVHKLYEGGVILPTN---FLSKIAPIVKEIFETDGEQFLKYPKPKVMQVDSAWMTD 356
 QY 383 EBFAREMLAGNPILLIRLEAPPTSKLDPNVGNQNSTITEEHKGLDGLTVDEAMKQ 442
 DB 357 EBFARETIAGLNPNVIKIEEPFLSKLDTOAGSDHTCIIAKEHLEPNLGLTLVEQAION 416
 QY 443 NRIYIVDHDALMPEYLTRMNTSTKYATRTLLKDDGTLKPLVIELALHPQDQDLGA 502
 DB 417 KGLFLDHDHYLIPYLRKINANTTYATRTIFFLKDDGTLTFLAIELSKHPQEGEYGP 476
 QY 503 ISKLYPPAENGQKSIWQLAKAYTVNDVGVHQLISHMLHVALEPFIATHROLSLVH 562
 DB 477 VSEVYVPASEGVEAVIWLAKAYVVVNDACYHQIISHWLSTHAIVEPFIATHROLVSVH 536
 QY 563 PIHKLLVPHYKDTMFINASARQVLINAGLITETHYPSKYSMELSSILYKOWTFPDQALP 622
 DB 537 PIYKLLFPHYRDTMINSARKALVNDAGIIEKTFMGKYSWEMSAVIYKOWTFPDQALP 596
 QY 623 NNLMKREGLAVEDSSAPHLRLINDYPAVDGLDIWSAIKTWQDYCYCLYYKDDNAVQND 682
 DB 597 NDLVKEGVAVKPSAPHGVRLLIEDYPYASDGLIWDIAKSWVQSVYFYSKDELOKD 656
 QY 683 FELQSWNNELEKGHADKKEHPWPKMQLTSLIESCTTIIWIASALHAANVFGOPYGG 742
 DB 657 PELQAWKKELVGEGDLKDEWQKQVTRFELVEASAILIWIASALHAANVFGOPYGG 716
 QY 743 YILNRPTTSRRFMFVGTAYEYKELESNPEKALRTICSELOALVSIISIIILSKHASDEV 802
 DB 717 LIILNRPTISRRFMFPEKSGSPYDALAKNPEKFLKITGKKTIDLTIVIELSRHASDEF 776
 QY 803 YLGQASID-WTSDKIALAEAFKPKGNLFVENRNRMERKNVKNRSGVNLPTLLVP 861
 DB 777 YLGQDGGDYWTSDAGPLEAFKFRFGKLEIEKLEKLEKLEKLEKLEKLEKLEKLEKLE 836
 QY 862 SSNEGTLTGSPNLSISI 878
 DB 837 SSEEGLTFRGIPNSISI 853

RESULT 12

LOX1 SOYBN
 ID LOX1 SOYBN STANDARD; PRT; 839 AA.
 AC P08170;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
 DE Seed lipoxygenase-1 (EC 1.13.11.12) (L-1).
 GN LOX1.1 OR LOX1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID:3847;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87280024; PubMed=3112136;
 RA Shibata D., Steczko J., Dixon J.E., Hermodson M., Yazdanparast R.,
 RA Axelrod B.;
 RT "Primary structure of soybean lipoxygenase-1.";
 RL J. Biol. Chem. 262:10080-10085 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Bonminor; TISSUE=Cotyledon;
 RA Fukazawa C., Masayoshi M., Chikafusa F.;
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 426-752 FROM N.A.
 RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,
 RA Altschuler M.;
 RT "Two soybean seed lipoxygenase nulls accumulate reduced levels of
 RT lipoxygenase transcripts.";
 RL Plant Mol. Biol. 7:11-23 (1986).
 RN [4]
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES, AND REVISIONS TO 479-482.
 RX MEDLINE=92232702; PubMed=1567851;
 RA Steczko J., Donoho G.P., Clemens J.C., Dixon J.E., Axelrod B.;
 RT "Conserved histidine residues in soybean lipoxygenase: functional
 RT consequences of their replacement.";
 RL Biochemistry 31:4053-4057 (1992).
 RN [5]
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES.
 RX MEDLINE=92360013; PubMed=1497657;
 RA Steczko J., Axelrod B.;
 RT "Identification of the iron-binding histidine residues in soybean
 RT lipoxygenase L-1.";
 RL Biochem. Biophys. Res. Commun. 186:686-689 (1992).
 RN [6]
 RP ACTIVE SITE, AND IRON LIGANDS.
 RX MEDLINE=93298753; PubMed=8518276;
 RA Minor W., Steczko J., Bolin J.T., Otwinowski Z., Axelrod B.;
 RT "Crystallographic determination of the active site iron and its
 RT ligands in soybean lipoxygenase L-1.";
 RL Biochemistry 32:6320-6323 (1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=93276267; PubMed=8502991;
 RA Boyington J.C., Gaffney B.J., Amzel L.M.;
 RT "The three-dimensional structure of an arachidonic acid
 RT 15-lipoxygenase.";
 RL Science 260:1482-1486 (1993).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RX MEDLINE=96346062; PubMed=8718858;
 RA Minor W., Steczko J., Stec B., Otwinowski Z., Bolin J.T., Walter R.,
 RA Axelrod B.;
 RT "Crystal structure of soybean lipoxygenase L-1 at 1.4-A resolution.";
 RL Biochemistry 35:10687-10701 (1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RX MEDLINE=21305677; PubMed=11412104;
 RA Tomchick D.R., Phan P., Cymborowski M., Minor W., Holman T.R.;
 RT "Structural and functional characterization of second-coordination
 RT sphere mutants of soybean lipoxygenase-1.";
 RL Biochemistry 40:7509-7517 (2001).
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
 CC WOUNDING. WITH LINOLEATE AS SUBSTRATE, L-1 SHOWS A PREFERENCE FOR

CARBON 13 AS THE SITE FOR HYDROPEROXIDATION (IN CONTRAST TO L-2
 AND L-3 WHICH UTILIZE EITHER CARBON 9 OR 13).
 -!- CATALYTIC ACTIVITY: linoleate + O(2) = (9Z,11E) - (13S) -13-
 hydroperoxyoctadeca-9,11-dienoate.
 -!- COFACTOR: Iron, one atom tightly bound per molecule.
 -!- SUBUNIT: Monomer.
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
 -!- INDUCTION: THE HYDROPEROXIDE PRODUCT SERVES TO ACTIVATE THE
 RESTING ENZYME. THE ACTIVATION IS ACCOMPANIED BY THE OXIDATION
 OF FE(2+) ENTADIENE STRUCTURE. L-1 PREFERENCES ANIONIC SUBSTRATE.
 -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
 L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
 ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
 -!- SIMILARITY: Belongs to the lipoxygenase family.
 -!- SIMILARITY: Contains 1 PLAT domain.
 -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 663
 TO 697 DUE TO A FRAMESHIFT.

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EMBL; J02795; AAA33986.1; -
 EMBL; X67304; CAA47717.1; ALT_FRAME.
 PIR; S25064; DASYL2.
 PDB; 1F8N; 04-JUL-01.
 PDB; 1FGN; 24-OCT-01.
 PDB; 1FGO; 04-JUL-01.
 PDB; 1FGQ; 04-JUL-01.
 PDB; 1FGR; 18-JUL-01.
 PDB; 1FGT; 04-JUL-01.
 PDB; 1YGE; 23-JUL-97.
 PDB; 2SBL; 27-FEB-95.
 InterPro; IPR000907; Lipoxygenase.
 InterPro; IPR001024; Lipoxygenase_LH2.
 InterPro; IPR008976; PLAT_LH2.
 Pfam; PF00305; lipoxygenase; 1.
 Pfam; PF01477; PLAT; 1.
 PRINTS; PR00087; LIPOXYGENASE.
 SMART; SM00308; LH2; 1.
 PROSITE; PS00711; LIPOXYGENASE_1; 1.
 PROSITE; PS00081; LIPOXYGENASE_2; 1.
 PROSITE; PS50095; PLAT; 1.
 Oxidoreductase; Dioxigenase; Iron; Multigene family; 3D-structure.
 DOMAIN 16 145
 METAL 499 499
 METAL 504 504
 METAL 690 690
 METAL 839 839
 MUTAGEN 494 494
 MUTAGEN 494 494
 MUTAGEN 499 499
 MUTAGEN 504 504
 MUTAGEN 517 517
 MUTAGEN 522 522
 MUTAGEN 531 531
 MUTAGEN 690 690
 CONFLICT 426 427
 CONFLICT 558 560
 CONFLICT 572 574
 CONFLICT 641 641
 CONFLICT 741 748
 STRAND 7 16
 HELIX 17 19
 TURN 20 20
 TURN 24 26
 HELIX 32 35
 TURN 37 38
 STRAND 40 50

LPS -> AL (IN REF. 3).
 KNW -> EL (IN REF. 3).
 N -> P (IN REF. 3).
 KLPTLISL -> SCRLSLAV (IN REF. 3).

FT	TURN	52	53	
FT	STRAND	56	58	
FT	STRAND	62	63	
FT	STRAND	66	68	
FT	TURN	76	77	
FT	STRAND	79	86	
FT	HELIX	89	91	
FT	STRAND	94	101	
FT	STRAND	107	114	
FT	TURN	117	120	
FT	STRAND	123	131	
FT	STRAND	133	133	
FT	HELIX	134	136	
FT	STRAND	141	144	
FT	HELIX	151	153	
FT	HELIX	156	158	
FT	HELIX	159	170	
FT	TURN	179	180	
FT	STRAND	186	187	
FT	STRAND	189	189	
FT	TURN	195	197	
FT	HELIX	199	201	
FT	STRAND	206	206	
FT	STRAND	217	218	
FT	STRAND	224	224	
FT	TURN	229	230	
FT	STRAND	232	232	
FT	HELIX	242	244	
FT	HELIX	251	253	
FT	HELIX	255	257	
FT	HELIX	258	264	
FT	TURN	265	265	
FT	HELIX	266	275	
FT	TURN	276	277	
FT	HELIX	286	290	
FT	HELIX	291	293	
FT	TURN	294	295	
FT	STRAND	297	298	
FT	HELIX	301	307	
FT	TURN	308	309	
FT	TURN	311	312	
FT	HELIX	313	316	
FT	STRAND	318	319	
FT	STRAND	324	326	
FT	HELIX	331	333	
FT	HELIX	339	341	
FT	HELIX	343	352	
FT	TURN	356	357	
FT	STRAND	360	361	
FT	HELIX	373	376	
Query Match 55.2%; Score 2582.5; DB 1; Length 839;				
Best Local Similarity 58.7%; Pred.No. 2.6e-168;				
Matches 497; Conservative 124; Mismatches 208; Indels 17; Gaps 8;				
QY	39	GNKIKGKVLMSNVLDTEPHSNLLDNFTLLGGVVSFQISATHSTNDSRGKVGKAY	98	
DB	5	GHKIKGTVVLPKNEVNP-DGSAVDNLNLFGRSVSLQLISATKADAGKGVKDTF	63	
QY	99	LERWLTSIPPLPAGESVPOINQWENFGFPDGAFFIKNGHTSEPFKLSLTLDVPGYGRV	158	
DB	64	LEGINTSLTLGAGESAFNIHFEWDGSMGIPGAFYIKRYMQVEFFKLSLTLEASNQGTI	123	
QY	159	HPDCSNWVYPSGRYKDKDRFFANHYVLPSONPLRKYREBELNWLKDGTEGKEWDRI	218	
DB	124	RVCNSWNTNKLKSVRFFANHYVLPSETAPLVSREBELKSLRNGTGERKEYDRI	183	
QY	219	YDYVYNDIADPDVGDH--RPILGGTTEYPPRRGRTGRPRRRDHNYESRLSPMSLDI	276	
DB	184	YDYVYNDLGNPKSEKLARPVLGGSSTPPYPRGRTGRGPTVDPNTEKQ-----GEVF	238	
QY	277	YVPCDNFGLKMSDFLGYTLKALSISIKPGLQSIDV--TPNEFDNFKVDNLFPERGFP	334	

DB	239	YVPRDENLHLSKDALEIGTKLSQIVQPAFESAFDLKSTPIEFHSPQDHYDLYEGGK	298	
QY	335	IPFNAFKTLTDLTPPLFKALVRNDGEKFLFPTPEVVVKDNKIGWSTDEEPAREMLAGPN	394	
DB	299	LPDRVISTI---IPLPVIKELYRTDGOHILFPPQPHVVQVSQSAWMTDEEPAREMIAGVN	355	
QY	395	PLLRLEAPPTSKLDPNVYGNQNSTTEBHIKGLDGLTVDEAMKONRLYIYVDFHDAL	454	
DB	356	PCVIRGLEFPKSNLDPAIYGDQSSKITADSL--DLDDGYTMDAELGSRRLFLMDYHDF	413	
QY	455	MPYLTRMN-ATSTKYATRTLLLLKDDGTLKPLVTELALPHPQGDOLGAISKLYPPAENG	513	
DB	414	MPYVQINQINSAKYATRTLLFLREDGTLKPALELSLPHSAGDLSAAVSQVVLPAKEG	473	
QY	514	VOKSIWQLAKAYTVNDVGYHQLISHWLTHAVLEFPFVIATHRQLSVLHPHKLIVPHYK	573	
DB	474	VESTIWLAKAYVIVNDSYHQLMSHNLNTHAAMPFVIATHRHLVSLHPYKLLTPHYR	533	
QY	574	DTMFNASARQVLINANGLIETHYPSKYSVELSILYKDWTFPDQALPNNIMKGLAVE	633	
DB	534	NNMNINALARQSLINANGIETTFLPKYSVEMSAVYKNNWFTDQALPADLIRKGVAIK	593	
QY	634	DGSAPHLRLINDYPFAVDGLDIWSAIKTWQDYCCLYYKDDNAVQNDFFELQSWNBLR	693	
DB	594	DPSTPHGVALLIEDYFAADGLEIWAIAIKTWQEVVPLYARFDDVDKNDSELQHWKEAV	653	
QY	694	EXGHADKXHEPWPQWQUTSELIESCTTIITATASALHAANFGQPYGYILNRTTSRR	753	
DB	654	EXGHGDLKDPWPKIQTLEDLVEVCLIIITATASALHAANFGQPYGYILNRTTSRR	713	
QY	754	FMPEVGTAEYKELESNPEKAFRTICSELQALVSISIIELLSKHASDEVYLGQRASIDWT	813	
DB	714	LUPEKGTPEYEEINNNHEKAYRTITSKLPITLSVIELLSTHASDEVYLGQRDNPHWT	773	
QY	814	SDKIALFAPEKFGKXNLFEVENRIMRNKEVNUK-NRSGPVNLPYLLVPSSNEGILTRGI	872	
DB	774	SDSKALQAFQKFKGLKEIEKLVRRNNDPSLQGNRLGFPVQLPYLLYPSSEGLTFRGI	833	
QY	873	PNSISI 878		
DB	834	PNSISI 839		
RESULT 13				
LOX1 LENCU STANDARD; PRT; 866 AA.				
AC	38414			
DT	01-OCT-1994	(Rel. 30, Created)		
DT	01-OCT-1994	(Rel. 30, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Lipoxygenase	(EC 1.13.11.12).		
GN	LOX1			
OS	Lens culinaris (Lentil).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Viciae; Lens.			
OX	NCBI_TaxID=3864;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Seedling shoot;			
RX	MEDLINE=94162308; PubMed=8117753;			
RA	Hilbers M.P., Rosel A., Finazzi-Agro A., Veldink G.A.,			
RA	Vliegenthart J.F.G.;			
RT	"The primary structure of a lipoxygenase from the shoots of etiolated			
RL	lentil seedlings derived from its cDNA."			
RL	Biochim. Biophys. Acta 1211:239-242(1994).			
CC	-i- FUNCTION. PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF			
CC	DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND			
CC	DEVELOPMENT, EST RESISTANCE, AND SENESENCE OR RESPONSES TO			
CC	WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING			
CC	A CIS, CIS-1,4-PENTADIENE STRUCTURE.			
CC	-i- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-			
CC	hydroperoxyoctadeca-9,11-dienoate.			

CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X71344; CAA50483.1; --
 CC HSP: P08170; 2SBL.
 CC InterPro: IPR000907; Lipoxigenase.
 CC InterPro: IPR01024; Lipoxigenase_LH2.
 CC InterPro: IPR008976; PLAT_LH2.
 CC Pfam: PF00305; lipoxigenase; 1.
 CC Pfam: PF01477; PLAT; 1.
 CC PRINTS: PR00087; LIPOXYGENASE.
 CC SMART: SM00308; LH2; 1.
 CC PROSITE: PS00711; LIPOXYGENASE_1; 1.
 CC PROSITE: PS00081; LIPOXYGENASE_2; 1.
 CC PROSITE: PS50095; PLAT; 1.
 CC Oxidoreductase; Dioxigenase; Iron; Multigene family.
 CC DOMAIN 42 171
 CC METAL 526 526 IRON (BY SIMILARITY).
 CC METAL 531 531 IRON (BY SIMILARITY).
 CC METAL 717 717 IRON (BY SIMILARITY).
 CC METAL 866 866 IRON (BY SIMILARITY).
 CC SEQUENCE 866 AA; 96638 MW; E3E5D00E94E3C89C CRC64;

Query Match 54.5%; Score 2546; DB 1; Length 866;
 Best Local Similarity 56.0%; Pred No. 8.3e-166;

Matches 486; Conservative 135; Mismatches 209; Indels 38; Gaps 8;

QY 39 GNKIKGVILMRNSVLDPT-----EFHSLNLFNTELLGGVSFQ 78
 DB 9 GQKLGTVILMKXVLDINALTAQAQSPGIIAGFVGVGSIAGSIIDTATAFGRSVLR 68
 QY 79 LISATHTNSDRSGKVKAYLERMLTSIPPLFAGESVFQINFDENFGPFGAFIKX-G 137
 DB 59 LISATVADASGKVKSEAFLEGULTSIPTLGDQSAFSEHFEDSNKNGTGFAGFIENFM 128
 QY 138 HTSEFFLKSLLDDVPGYGRVHFDCNSWVPSGKYKDRIPFANHVLPISQTNPLKRYR 197
 DB 129 QGGEFFLVSLDDVPVNGSIKFAKNSWYNDKXVQSDRIPFANKTYPATAPLVSYR 188
 QY 198 BEELWNLRGDTGERKEWDRIYDVNDIADPP-----VGDHRIPLGGTTEYPYPRGRGT 253
 DB 189 QEEELTURGDTGERQEWDRIDYDVNDLGPAPQKATLG--RVLPGSSSTLPYPRGRGT 246
 QY 254 GRPSRRDHYESRLSPIMSLDIYVPDENFGHLMKMSDFILGYTLKALSISIKPGLOSPID 313
 DB 247 GRKXTVKEPQESR-----SDTVLPDRDEAFGHVKSSDFLVILKASQNIYVQLRSVVT 301
 QY 314 VTPN--EEDNPKVDNLPFERGPIPFNAKFTLTEDLPPLFKALVRNDGKFLKFPPTPEV 371
 DB 302 LQLANPEFTEDVRSYLDGKILPTDVLKIS---DIPLFSELSFSDGEALKFPFPKV 358
 QY 372 VKDKKIGHSTDEEFAREMLAGNPLLRLEAFPTSKLPDNYVGNQNSITTEHKHGL 431
 DB 359 IQVDHSAWTEDEEFAREMIAGNPHILKEVLSFPIKSKLDQSGYVGMTSKITKEHLEPNL 418
 QY 432 DGLTVDAMKNRLYIVDFHDALMPYLRMKNATSKTYATRTLLIXDDGTLKPLVIELA 491
 DB 419 GGVTVGAIQTNRLFTPDHDLFPYLRKINATKAYATRTVLFLQDNGTLKPLALELS 478
 QY 492 LPHPQGLGAIKLYPFAENGOKSWOLAKAVTVNDVGVHQLSHWLTHTAVLEPFFV 551
 DB 479 TPHPDGDGFGPVSKVYLPASEGVEASIWLLAKAFVWVNDSCYHQLVSHWLTHTAVVEPFI 538

QY 552 IATHRQLSVLHPHKLVLPHYKDTMTFINASARQVLINANGLIETTHYPYSKYSMELSSILY 611
 DB 539 IATNRHLSVHPHKLVLPHYKDTMTFINALARNVLVNAEGIIETSTLWNGYANEMSAVY 598
 QY 612 KDWTFFDQALPNNLMKRGIAVEDSSAPHGRLILINDYPFAVDGLDIWSAIKTWQDYCCCL 671
 DB 599 KDWFFDQGLFNDLIKRGVAVKDPSPHGVRLIEDYPYASDGLLEWAAIKSWVEEYVNF 658
 QY 672 YYKDDNAVQNDFFELQSWNNELEKSHADKHPWPKMOTLSELIESCTTIWIASALHA 731
 DB 659 YYKSDAAIAQDAELQAFKELVEVGHGDLKSAWTFKMQNRKELIACSLIWIASALHA 718
 QY 732 AVNFGQYPGYILNRPPTTSRRPMPVGTAYEKELESNPEKAPLRTICSELQALVSIISII 791
 DB 719 AVNFGQYPGYILNRPPTTSRRPMPKGTPEYDGLAKNYEKAYLRITITPKNDTLTDLTII 778
 QY 792 EILSKIASDEVILGOR-ASIDMTSKIALEAEKFGKNI-FEVENRIMERNKEVNLKNRSG 850
 DB 779 EVLSRHASDEQYLGRIEGDDMTTDSVPKEAFKFGKLABIEEKLQNRNDESLNRNG 838
 QY 851 PVNLPTLLVPSNEGLTGRGIPNSISI 878
 DB 839 PVKMPYTLVPSSEGLTCRGIPNSISI 866

RESULT 14

LOX1_HORVU STANDARD; PRT; 862 AA.
 ID LOX1_HORVU STANDARD; PRT; 862 AA.
 AC P29114; Q42845;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipoxigenase 1 (EC 1.13.11.12).
 GN LOX1.1 OR LOXA.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Triticeae; Hordeum.
 CC NCBI_TaxID=4513;
 CX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Triumph;
 RX MEDLINE=95127754; PubMed=7827128;
 RA van Mechelen J.R., Smits M., Douma A.C., Rouster J., Cameron-Mills V.,
 RA Heidekamp F., Valk B.E.;
 RT "Primary structure of a lipoxigenase from barley grain as deduced
 RT from its cDNA sequence.";
 RL Biochim. Biophys. Acta 1254:221-225(1995).
 [2]
 RN SEQUENCE OF 274-294 AND 832-845.
 RP STRAIN=cv. Triumph; TISSUE=Embryo;
 RX MEDLINE=92207997; PubMed=1554746;
 RA Doderer A., Kokkelink I., van der Veen S., Valk B.E., Schram A.W.,
 RA Douma A.C.;
 RT "Purification and characterization of two lipoxigenase isoenzymes
 RT from germinating barley.";
 RL Biochim. Biophys. Acta 1120:97-104(1992).
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 CC hydroperoxyoctadeca-9,11-dienoate.
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
 CC -!- SUBUNIT: Monomer.
 CC -!- DEVELOPMENTAL STAGE: IN BOTH QUIESCENT AND GERMINATING SEEDS.
 CC -!- MISCELLANEOUS: WITH LINOLEATE AS SUBSTRATE, LIPOXYGENASE 1 SHOWS A
 CC SPECIFICITY FOR CARBON 9 AS THE SITE FOR HYDROPEROXIDATION (IN
 CC CONTRAST TO LIPOXYGENASE 2, WHICH SHOWS A PREFERENCE FOR CARBON
 CC 13).
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.

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